

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 23, 2006, 07:43:54 ; Search time 38 Seconds
(without alignments)
238.010 Million cell updates/sec

Title: US-09-688-566-81
Perfect score: 494
Sequence: 1 VSDPRDLVVAAPTSLRI.....VTDKSDTYKYDDPISINVRT 94

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	361	73.1	2386	1 FNHU	fibronectin precur
2	354	71.7	2265	1 FNBO	fibronectin - bovi
3	333	67.4	2477	2 S14428	fibronectin precu
4	311	63.0	273	2 A28512	fibronectin - chic
5	311	63.0	1020	2 A29355	fibronectin - chic
6	262	53.0	2481	2 A43908	fibronectin - Afri
7	125	25.3	4005	2 T09070	probable tenascin
8	124	25.1	4135	2 T42629	tenascin-X - bovin
9	121	24.5	1353	1 JH0675	restriclin precurs
10	121	24.5	1746	1 S19694	tenascin precursor
11	116	23.5	1356	2 A45445	janusin precursor,
12	111	22.5	3566	1 A40701	tenascin-X precurs
13	110.5	22.4	1898	2 S46216	leukocyte antigen-
14	110	22.3	2019	1 JQ1322	tenascin precursor
15	108	21.9	933	2 A31930	cytotactin - chick
16	108	21.9	1810	1 A32230	tenascin precursor
17	106.5	21.6	2944	2 A54849	collagen alpha 1(V
18	105	21.3	2201	2 A32160	tenascin-X - pig (
19	102	20.6	417	2 S65944	protein-tyrosine-p
20	100	20.2	1912	2 A56178	tenascin - eastern
21	98.5	19.9	647	2 A43902	leucocyte common a
22	96	19.4	1290	2 A56493	collagen alpha 1(X
23	96	19.4	3124	2 A40020	undulin 1 - human
24	94	19.0	843	2 A40970	protein-tyrosine-p
25	92	18.6	1691	1 D54689	protein-tyrosine-p
26	92	18.6	1894	2 C54689	fibronectin, trans
27	91.5	18.5	147	2 S00848	protein-tyrosine-p
28	90.5	18.3	440	2 I50213	fibronectin - chic
29	88.5	17.9	189	2 S71465	

ALIGNMENTS

RESULT 1

FNHU

fibronectin precursor [validated] - human
N;Alternate names: fibronectin splice form ED-A

C;Species: Homo sapiens (man)

C;Date: 27-Nov-1985 #sequence revision 31-Mar-1993 #text change 31-Dec-2004

C;Accession: A26460; A26284; S03917; A24854; A24476; A91008; A93529; A21011; A90495; A22

R;Dean, D.C.; Bowlin, C.L.; Bourgeois, S.

Proc. Natl. Acad. Sci. U.S.A. 84, 1876-1880, 1987

A;Title: Cloning and analysis of the promoter region of the human fibronectin gene.

A;Reference number: A26460; MUID:87175578; PMID:3031656

A;Accession: A26460

A;Molecule type: DNA

A;Residues: 1-49 <DEA>

A;Cross-references: UNIPROT:P02751; UNIPROT:Q14327; UNIPARC:UPI000016A926; GB:M15801; NI

R;Oldberg, A.; Ruoslahti, E.

J. Biol. Chem. 261, 2113-2116, 1986

A;Title: Evolution of the fibronectin gene.

A;Reference number: A26284; MUID:86111901; PMID:3003095

A;Accession: A26284

A;Molecule type: DNA

A;Residues: 1447-1540 <OLD>

A;Cross-references: UNIPARC:UPI0000112E37; GB:M12549; NID:g182688

A;Note: the authors translated the codon TTC for residue 1494 as Glu

R;Paolella, G.; Henschcliff, C.; Sebastio, G.; Baralle, F.E.

Nucleic Acids Res. 16, 3545-3557, 1988

A;Title: Sequence analysis and in vivo expression show that alternative splicing of ED-B

A;Reference number: S00848; MUID:88233940; PMID:3375063

A;Accession: S03917

A;Molecule type: DNA

A;Residues: 1594-1767, 'V', 1769-1783 <PAO>

A;Cross-references: UNIPARC:UPI000017432B; EMBL:X07718; NID:g31402

A;Note: the authors translated the codon AAC for residue 1631 as Asp

R;Vibe-Pedersen, K.; Magnusson, S.; Baralle, F.E.

FEBS Lett. 207, 287-291, 1986

A;Title: Donor and acceptor splice signals within an exon of the human fibronectin gene:

A;Reference number: A24854; MUID:87030929; PMID:3770201

A;Accession: A24854

A;Molecule type: DNA

A;Residues: 1992-2147 <VIB>

A;Cross-references: UNIPARC:UPI000017432C; GB:X04530; NID:g31436

R;Gutman, A.; Yamada, K.M.; Kornblihtt, A.

FEBS Lett. 207, 145-148, 1986

A;Title: Human fibronectin is synthesized as a pre-propolypeptide.

A;Reference number: A24476; MUID:87030890; PMID:3770189

A;Accession: A24476

A;Status: not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-14, 'Q', 16-38 <GUT>

A;Cross-references: UNIPARC:UPI000017432D

R;Kornblihtt, A.R.; Umezawa, K.; Vibe-Pedersen, K.; Baralle, F.E.

EMBO J. 4, 1755-1759, 1985

tenascin - rat (fr
fibronectin ED-B -
leukocyte antigen-
protein-tyrosine-p
tenascin-X - mouse
fibronectin ED-A -
nephlin - human
type XII collagen
collagen alpha 1(X
collagen alpha 1(X
collagen alpha 1(X
tenascin Y precurs
protein-tyrosine-p
protein-tyrosine-p
undulin 2 - human
hypothetical prote

A;Title: Primary structure of human fibronectin: differential splicing may generate at l
A;Reference number: A91008; MUID:85284965; PMID:2952939
A;Accession: A91008
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 32-1344, 1346-2080,2112-2386 <KOR>
A;Cross-references: UNIPARC:UPI000017432E; UNIPARC:UPI000017433F; GB:X02761
R;Kornblitt, A.R.; Vibe-Pedersen, K.; Baralle, F.E.
Nucleic Acids Res. 12, 5853-5868, 1984
A;Title: Human fibronectin: cell specific alternative mRNA splicing generates polypeptid
A;Reference number: A93529; MUID:84272258; PMID:6462919
A;Accession: A93529
A;Molecule type: mRNA
A;Residues: 973-2080;2112-2386 <X02>
A;Cross-references: UNIPARC:UPI000017432F; UNIPARC:UPI0000174330; GB:X00739
R;Oldberg, A.; Linney, E.; Ruoslahti, E.
J. Biol. Chem. 258, 10193-10196, 1983
A;Title: Molecular cloning and nucleotide sequence of a cDNA clone coding for the cell a
A;Reference number: A21011; MUID:83230929; PMID:6688418
A;Accession: A21011
A;Molecule type: mRNA
A;Residues: 1434-1537 <OL2>
A;Cross-references: UNIPARC:UPI0000174331; GB:X00055; NID:g182680; PIDN:AAAS2459.1; PID:
R;Bernard, M.P.; Kolbe, M.; Weil, D.; Chu, M.L.
Biochemistry 24, 2698-2704, 1985
A;Title: Human cellular fibronectin: comparison of the carboxyl-terminal portion with ra
A;Reference number: A90495; MUID:85280409; PMID:2992573
A;Accession: A90495
A;Molecule type: mRNA
A;Residues: 1594-2386 <BER>
A;Cross-references: UNIPARC:UPI000016A928; GB:M10905; NID:g182696; PIDN:AAAS2462.1; PID:
R;Umezawa, K.; Kornblitt, A.R.; Baralle, F.E.
FEBS Lett. 186, 31-34, 1985
A;Title: Isolation and characterization of cDNA clones for human liver fibronectin.
A;Reference number: A22245; MUID:85231203; PMID:2989004
A;Accession: A22245
A;Molecule type: mRNA
A;Residues: 1948-2067 <UME>
A;Cross-references: UNIPARC:UPI000000046A; GB:M27589; NID:g182705; PIDN:AAAS2465.1; PID:
A;Accession: B22245
A;Molecule type: mRNA
A;Residues: 1975-1991,2017-2039 <UM2>
A;Cross-references: UNIPARC:UPI0000174332; UNIPARC:UPI0000174333; GB:M27590
R;Sekiguchi, K.; Kioe, A.M.; Kurachi, K.; Yoshitake, S.; Hakomori, S.
Biochemistry 25, 4936-4941, 1986
A;Title: Human liver fibronectin complementary DNAs: identification of two different mes
A;Reference number: I52394; MUID:87026578; PMID:3021206
A;Accession: I65273
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1978-1990,2016-2018,'N',2020-2081,2113-2127 <SEK>
A;Cross-references: UNIPARC:UPI000006E04C; GB:M14060; NID:g182701; PIDN:AAAS2464.1; PID:
R;Kornblitt, A.R.; Vibe-Pedersen, K.; Baralle, F.E.
Proc. Natl. Acad. Sci. U.S.A. 80, 3218-3222, 1983
A;Title: Isolation and characterization of cDNA clones for human and bovine fibronectin
A;Reference number: A21165; MUID:83221567; PMID:6304699
A;Accession: A21165
A;Molecule type: mRNA
A;Residues: 2291-2386 <K03>
A;Cross-references: UNIPARC:UPI0000174334; GB:X00799; NID:g182681; PIDN:AAAS2460.1; PID:
R;Garcia-Pardo, A.; Pearlstein, E.; Frangione, B.
J. Biol. Chem. 258, 12670-12674, 1983
A;Title: Primary structure of human plasma fibronectin.
A;Reference number: A92398; MUID:84032463; PMID:6630202
A;Accession: A92398
A;Molecule type: protein
A;Residues: 32-47,'C',49-51,'S',53-72,'A',74-290 <GARI>
A;Cross-references: UNIPARC:UPI0000174335
R;Garcia-Pardo, A.; Gold, L.I.
Arch. Biochem. Biophys. 304, 181-188, 1993
A;Title: Further characterization of the binding of fibronectin to gelatin reveals the p
A;Reference number: S34791; MUID:93312001; PMID:8323285
A;Accession: S34791
A;Molecule type: protein
A;Residues: 291-300;551-560 <GAR2>
A;Cross-references: UNIPARC:UPI0000174336; UNIPARC:UPI0000174337
R;Griffin, C.A.; Calaycay, J.; Shively, J.E.; Smith, R.L.
Thromb. Res. 43, 469-477, 1986
A;Title: Two plasma fibronectin fragments with different gelatin-binding properties.
A;Reference number: A60904; MUID:87019725; PMID:3532418
A;Accession: A60904
A;Molecule type: protein
A;Residues: 293-301 <GRI>
A;Cross-references: UNIPARC:UPI0000174338
R;Calaycay, J.; Pande, H.; Lee, T.; Borsi, L.; Siri, A.; Shively, J.E.; Zardi, L.
J. Biol. Chem. 260, 12136-12141, 1985
A;Title: Primary structure of a DNA- and heparin-binding domain (domain III) in human pla
A;Reference number: A23901; MUID:86008277; PMID:3900070
A;Accession: A23901
A;Molecule type: protein
A;Residues: 616-677,'Q',679-703,'PT' <CAL>
A;Cross-references: UNIPARC:UPI0000174339
R;Pierschbacher, M.D.; Ruoslahti, E.; Sundelin, J.; Lind, P.; Peterson, P.A.
J. Biol. Chem. 257, 9593-9597, 1982
A;Title: The cell attachment domain of fibronectin. Determination of the primary structu
A;Reference number: A92386; MUID:82265604; PMID:7050098
A;Accession: A92386
A;Molecule type: protein
A;Residues: 1441-1548 <PIE>
A;Cross-references: UNIPARC:UPI0000141CD5
A;Note: residues 1524-1527 are responsible for the cell-binding activity
R;Garcia-Pardo, A.; Rostagno, A.; Frangione, B.
Biochem. J. 241, 923-928, 1987
A;Title: Primary structure of human plasma fibronectin. Characterization of a 38 kDa dom
A;Reference number: A32517; MUID:87241275; PMID:3593230
A;Accession: A32517
A;Molecule type: protein
A;Residues: 1589-1630,'T',1722-2058 <GAR3>
A;Cross-references: UNIPARC:UPI000017433A
R;Fressel, T.; McCarthy, J.B.; Calaycay, J.; Lee, T.D.; Legesse, K.; Shively, J.E.; Pand
Biochem. J. 274, 731-738, 1991
A;Title: Human plasma fibronectin. Demonstration of structural differences between the A-
A;Reference number: S14357; MUID:91190085; PMID:2012601
A;Accession: S14357
A;Molecule type: protein
A;Residues: 1614-1630,'T',1722-2081,2113-2244 <TRE>
A;Cross-references: UNIPARC:UPI000017433B
R;Garcia-Pardo, A.; Pearlstein, E.; Frangione, B.
J. Biol. Chem. 260, 10320-10325, 1985
A;Title: Primary structure of human plasma fibronectin. Characterization of a 31,000-dalt
A;Reference number: A23891; MUID:85261459; PMID:4019516
A;Accession: A23891
A;Molecule type: protein
A;Residues: 2071-2080;2112-2356 <GAR4>
A;Cross-references: UNIPARC:UPI000017433C; UNIPARC:UPI000017433D
C;Comment: The extra domain and connecting strand 3 are subject to developmental and tiss
C;Comment: The cellular and plasma fibronectins are high molecular weight glycoproteins,
ation, and transformation.
C;Genetics:
A;Gene: GDB:FNI
A;Cross-references: GDB:119135; OMIM:135600
A;Map position: 2q34-q34
A;Introns: 49/3; 1266/1; 1357/1; 1447/1; 1487/1; 1541/1; 1631/1; 1721/1; 1991/1; 2145/1
C;Superfamily: fibronectin type I repeat homology; fibronectin type II repeat homology; f
C;Keywords: acute phase; alternative splicing; cell adhesion; collagen binding; duplicati
F;1-26/Domain: signal sequence #status predicted <SIS>
F;27-31/Domain: propeptide #status predicted <PRO>
F;32-2386/Product: fibronectin #status experimental <MAT>
F;52-272/Domain: fibrin and heparin binding <PHB>
F;52-87/Domain: fibronectin type I repeat homology <IP1>
F;97-135/Domain: fibronectin type I repeat homology <IF2>
F;141-179/Domain: fibronectin type I repeat homology <IF3>
F;186-225/Domain: fibronectin type I repeat homology <IF4>
F;231-270/Domain: fibronectin type I repeat homology <IF5>
F;308-608/Domain: collagen binding <CBR>
F;308-342/Domain: fibronectin type I repeat homology <IF6>

F;360-401/Domain: fibronectin type II repeat homology <2F1>
F;420-461/Domain: fibronectin type II repeat homology <2F2>
F;470-508/Domain: fibronectin type I repeat homology <1F7>
F;518-555/Domain: fibronectin type I repeat homology <1F8>
F;561-599/Domain: fibronectin type I repeat homology <1F9>

Query Match 73.1%; Score 361; DB 1; Length 2386;
Best Local Similarity 77.7%; Pred. No. 1.8e-28;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

QY 1 VSDVPRDLVVAATPTSLRLISWNRSLGQSYRYRITYTGTCGNSPVQSFVPPWASIIATIS 60
DB 1447 VSDVPRDLVVAATPTSLRLISWNRSLGQSYRYRITYTGTCGNSPVQSFVPPWASIIATIS 1506
QY 61 GLKPGVDYTTIVAVTDKSTPYKYDDPISINRYT 94
DB 1507 GLKPGVDYTTIVAVTGRGDSPPASSKPFISINRYT 1540

RESULT 2
FNBO
Fibronectin - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 31-Dec-1988 #sequence revision 31-Dec-1988 #text_change 09-Jul-2004
C;Accession: A26452; B21165; A23292
R;Skorstengaard, K.; Jensen, M.S.; Sahl, P.; Petersen, T.E.; Magnusson, S.
Eur. J. Biochem. 161, 441-453, 1986
A;Title: Complete primary structure of bovine plasma fibronectin.
A;Reference number: A26452; MUID:87054047; PMID:3780752
A;Accession: A26452
A;Molecule type: protein
A;Residues: 1-2265 <SKO>
A;Cross-references: UNIPROT:P07589; UNIPARC:UPI000012A7BE
R;Kornblitt, A.R.; Vibe-Pedersen, K.; Baralle, F.E.
Proc. Natl. Acad. Sci. U.S.A. 80, 3218-3222, 1983
A;Title: Isolation and characterization of cDNA clones for human and bovine fibronectin
A;Reference number: A21165; MUID:83221567; PMID:6304699
A;Accession: B21165
A;Molecule type: mRNA
A;Residues: 2170-2265 <KOR>
A;Cross-references: UNIPARC:UPI000016C30C; GB:K00800; NID:glC3055; PIDN:AAA30521.2; PID:
R;Petersen, T.E.; Thøgersen, H.C.; Skorstengaard, K.; Vibe-Pedersen, K.; Sahl, P.; Sottr
Proc. Natl. Acad. Sci. U.S.A. 80, 137-141, 1983
A;Title: Partial primary structure of bovine plasma fibronectin: three types of internal
A;Reference number: A23292; MUID:83117805; PMID:6218503
A;Accession: A23292
A;Molecule type: protein
A;Residues: 1-16,'C',18-20,'S',22-432;447-463;1367-1517;1567-1673;2062-2176,'N',2178-226
A;Cross-references: UNIPARC:UPI000017433E; UNIPARC:UPI000017433F; UNIPARC:UPI0000174340;
C;Comment: Cys-1201 and Cys-2015 have free sulfhydryl groups.
C;Comment: The plasma fibronectin molecule consists of two chains, which are connected b
C;Comment: Fibronectins bind cell surfaces and various compounds including collagen, fib
aling, and maintenance of cell shape.
C;Comment: Plasma fibronectin is synthesized by hepatocytes.
C;Superfamily: fibronectin; fibronectin type I repeat homology; fibronectin type II repe
C;Keywords: acute phase; alternative splicing; collagen binding; duplication; extracellu
F;21-241/Domain: fibrin and heparin binding <FBR>
F;21-56/Domain: fibronectin type I repeat homology <1F1>
F;66-104/Domain: fibronectin type I repeat homology <1F2>
F;110-148/Domain: fibronectin type I repeat homology <1F3>
F;155-194/Domain: fibronectin type I repeat homology <1F4>
F;200-239/Domain: fibronectin type I repeat homology <1F5>
F;277-577/Domain: collagen binding <CBR>
F;277-311/Domain: fibronectin type I repeat homology <1F6>
F;329-370/Domain: fibronectin type II repeat homology <2F1>
F;389-430/Domain: fibronectin type II repeat homology <2F2>
F;439-477/Domain: fibronectin type I repeat homology <1F7>
F;487-524/Domain: fibronectin type I repeat homology <1F8>
F;530-568/Domain: fibronectin type I repeat homology <1F9>
F;578-661/Domain: fibronectin type III repeat homology <FN3A>
F;688-770/Domain: fibronectin type III repeat homology <FN3B>
F;779-860/Domain: fibronectin type III repeat homology <FN3C>
F;875-957/Domain: fibronectin type III repeat homology <FN3D>

F;965-1046/Domain: fibronectin type III repeat homology <FN3E>
F;1055-1134/Domain: fibronectin type III repeat homology <FN3F>
F;1142-1227/Domain: fibronectin type III repeat homology <FN3G>
F;1235-1318/Domain: fibronectin type III repeat homology <FN3H>
F;1326-1404/Domain: fibronectin type III repeat homology <GN3I>
F;1410-1517/Domain: cell attachment <CAD>
F;1416-1502/Domain: fibronectin type III repeat homology <FN3J>
F;1493-1495/Domain: cell attachment (R-G-D) motif
F;1510-1592/Domain: fibronectin type III repeat homology <FN3K>
F;1600-1870/Domain: heparin binding <HB2>
F;1600-1682/Domain: fibronectin type III repeat homology <FN3L>
F;1692-1773/Domain: fibronectin type III repeat homology <FN3M>
F;1781-1863/Domain: fibronectin type III repeat homology <FN3N>
F;1970-1972/Region: cell attachment (R-G-D) motif
F;1982-2062/Domain: fibronectin type III repeat homology <FN3O>
F;1985-2216/Domain: fibrin binding <FB2>
F;2085-2124/Domain: fibronectin type I repeat homology <1F10>
F;2130-2167/Domain: fibronectin type I repeat homology <1F11>
F;2174-2209/Domain: fibronectin type I repeat homology <1F12>
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;3/Cross-link: isopeptide (Gln) (interchain to Lys N6-amino of fibrin) #status experime
F;21-47,45-56,66-94,92-104,110-138,136-148,155-184,182-194,200-229,227-239,277-304,302-3
7,2155-2167,2174-2200,2198-2209/Disulfide bonds: #status predicted
F;339,497,511,846,976,1213,1987/Binding site: carbohydrate (Asn) (covalent) #status expe
F;1205,1692/Binding site: carbohydrate (Asn) (covalent) #status absent
F;1943,1944/Binding site: carbohydrate (Thr) (covalent) #status experimental
F;2246/Disulfide bonds: interchain (to 2250) #status predicted
F;2250/Disulfide bonds: interchain (to 2246) #status predicted
F;2263/Binding site: phosphate (Ser) (covalent) #status experimental

Query Match 71.7%; Score 354; DB 1; Length 2265;
Best Local Similarity 74.5%; Pred. No. 8.8e-28;
Matches 70; Conservative 7; Mismatches 17; Indels 0; Gaps 0;

QY 1 VSDVPRDLVVAATPTSLRLISWNRSLGQSYRYRITYTGTCGNSPVQSFVPPWASIIATIS 60
DB 1416 VSDVPRDLVVAATPTSLRLISWNRSLGQSYRYRITYTGTCGNSPVQSFVPPWASIIATIS 1475
QY 61 GLKPGVDYTTIVAVTDKSTPYKYDDPISINRYT 94
DB 1476 GLKPGVDYTTIVAVTGRGDSPPASSKPFVSINRYT 1509

RESULT 3
S14428
Fibronectin precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Oct-1994 #sequence revision 28-Oct-1994 #text change 09-Jul-2004
C;Accession: S14428; S12455; A22319; S46203; S00459; A27252; I59049
R;Hynes, R.O.
Submitted to the EMBL Data Library, July 1989
A;Reference number: S14428
A;Accession: S14428
A;Molecule type: mRNA
A;Residues: 1-2477 <HYN>
A;Cross-references: UNIPROT:P04937; UNIPARC:UPI000012A7C6; EMBL:X15906; NID:g56163; PIDN:
R;Schwarzbauer, J.E.; Patel, R.S.; Fonda, D.; Hynes, R.O.
EMBO J. 6, 2573-2580, 1987
A;Title: Multiple sites of alternative splicing of the rat fibronectin gene transcript.
A;Reference number: S12455; MUID:88054951; PMID:2445560
A;Accession: S12455
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 609-1810,'T',1812-2283 <SCH>
A;Cross-references: UNIPARC:UPI0000177AEA; EMBL:X15906
R;Tamkun, J.W.; Schwarzbauer, J.E.; Hynes, R.O.
Proc. Natl. Acad. Sci. U.S.A. 81, 5140-5144, 1984
A;Title: A single rat fibronectin gene generates three different mRNAs by alternative sp
A;Reference number: A22319; MUID:84238097; PMID:6089177
A;Accession: A22319
A;Molecule type: DNA
A;Residues: 2052-2237 <TAM>
A;Cross-references: UNIPARC:UPI0000177AEB

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-4135 <ELB>

A;Cross-references: UNIPROT:O18977; UNIPARC:UPI00001101C4; EMBL:Y11915; NID:g2462978; PIDN:

C;Genetics:

A;Gene: TN-X

C;Superfamily: tenascin-X; EGF homology; fibrinogen beta/gamma homology; fibronectin type

C;Keywords: extracellular matrix; glycoprotein; heptad repeat

Query Match 25.1%; Score 124; DB 2; Length 4135;
Best Local Similarity 35.9%; Pred. No. 0.00065;
Matches 33; Conservative 17; Mismatches 36; Indels 6; Gaps 3;

QY 3 DVPRDLVVAATPTSLISNRSLGQSRYYRITYGETGNSPVQETVPPWASIAIISGL 62

DB 840 DGPQDLVVAATPTTLELWLRPQAEVDFVVSYS-VSAGNQVR-LEVFSQADGTLTLGL 897

QY 63 KPGVDYITIVYAVTDKSDTYKDDPISINYRT 94

DB 898 MPGVEYVTVTAERGRAVSY-----PASIRANT 925

RESULT 9

JH0675

restrictin precursor - chicken

C;Species: Gallus gallus (chicken)

C;Date: 10-Sep-1999 #sequence.revision 10-Sep-1999 #text_change 09-Jul-2004

C;Accession: JH0675; PS0385; S23254

R;Noerenberg, U.; Wille, H.; Wolffe, J.M.; Frank, R.; Rathjen, F.G.

Nuclon 8, 849-863, 1992

A;Title: The chicken neural extracellular matrix molecule restrictin: similarity with EG

A;Reference number: JH0675; MUID:92265298; PMID:1375037

A;Accession: JH0675

A;Molecule type: mRNA

A;Residues: 1-1353 <NOE>

A;Cross-references: UNIPROT:Q00546; UNIPARC:UPI00000FC0A7; GB:X64649; NID:g63613; PIDN:

A;Experimental source: brain

A;Accession: PS0385

A;Molecule type: protein

A;Residues: 579-586;827-840 <NOEL>

A;Cross-references: UNIPARC:UPI0000174344; UNIPARC:UPI0000174345

C;Comment: This protein is a neural extracellular matrix protein implicated in neural ce

C;Superfamily: restrictin; EGF homology; fibrinogen beta/gamma homology; fibronectin typ

C;Keywords: calcium binding; cell adhesion; duplication; extracellular matrix; glycopro

F;1-33/Domain: signal sequence #status predicted <SIG>

F;203-229/Product: restrictin #status predicted <MAT>

F;234-260/Domain: EGF homology <EG1>

F;265-291/Domain: EGF homology <EG2>

F;296-322/Domain: EGF homology <EG3>

F;324-405/Domain: EGF homology <EG4>

F;413-494/Domain: fibronectin type III repeat homology <FN1>

F;502-584/Domain: fibronectin type III repeat homology <FN2>

F;592-676/Domain: fibronectin type III repeat homology <FN3>

F;684-764/Domain: fibronectin type III repeat homology <FN4>

F;772-853/Domain: fibronectin type III repeat homology <FN5>

F;861-949/Domain: fibronectin type III repeat homology <FN6>

F;949-1027/Domain: fibronectin type III repeat homology <FN7>

F;1035-1115/Domain: fibronectin type III repeat homology <FN8>

F;1130-1338/Domain: fibronectin type III repeat homology <FN9>

F;1272-1286/Region: calcium binding #status predicted

F;1397-277,391,469,580,734,790,960,1031,1041,1236,1342/Binding site: carbohydrate (Aer

Query Match 24.5%; Score 121; DB 1; Length 1353;

Best Local Similarity 40.3%; Pred. No. 0.00037;

Matches 29; Conservative 13; Mismatches 28; Indels 2; Gaps 1;

QY 3 DVPRDLVVAATPTSLISNRSLGQSRYYRITYGETGNSPVQETVPPWASIAIISGL 62

DB 686 DSPRDLVLVASTSTSLSWTKAMGPIDYRVTF--TPASGMASEVTVSRNESQLTSEL 743

QY 63 KPGVDYITIVYA 74

submitted to the EMBL Data Library, November 1992

A;Description: Molecular characterization and in situ mRNA localization of the neural re

A;Reference number: S32023

A;Accession: S32023

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-1356 <FUS2>

A;Cross-references: UNIPARC:UPI000006D8A; EMBL:Z18630; NID:g57961; PIDN:CAA79229.1; PID

C;Superfamily: restrictin; EGF homology; fibrinogen beta/gamma homology; fibronectin ty

C;Keywords: alternative splicing; duplication; fibronectin type III repeat homology; olig

F;1-1356/Product: janusin, long form #status experimental <ALT>

F;1-772,863-1356/Product: janusin, short form #status experimental <ALT>

F;204-230/Domain: EGF homology <EG1>

F;235-261/Domain: EGF homology <EG2>

F;266-292/Domain: EGF homology <EG3>

F;297-323/Domain: EGF homology <EG4>

F;325-405/Domain: fibronectin type III repeat homology <FN1>

F;413-494/Domain: fibronectin type III repeat homology <FN2>

F;502-584/Domain: fibronectin type III repeat homology <FN3>

F;592-676/Domain: fibronectin type III repeat homology <FN4>

F;684-764/Domain: fibronectin type III repeat homology <FN5>

F;772-854/Domain: fibronectin type III repeat homology <FN6>

F;1038-1118/Domain: fibronectin type III repeat homology <FN7>

F;1133-1341/Domain: fibrinogen beta/gamma homology <FBG>

Query Match 23.5%; Score 116; DB 2; Length 1356;

Best Local Similarity 27.4%; Pred. No. 0.0012;

Matches 34; Conservative 18; Mismatches 36; Indels 36; Gaps 3;

QY 3 DVPRDLVVAATPTSLRSLWNRSGLQSYRYITVGETGNSPVQVFTVPPWASIIATISGL 62

DB 686 DSPRLDMVTASSETSLIWTKASGPIDHYRITPTSSGIS--SEVTVPRDRGTSYTUTDL 743

QY 63 KPGVDYITVYA-----VTDKSDTYKYDDP-----I 88

DB 744 EPGAEEYIISITAEGRQOOSLESTVDAFTGPRFPIHLHFHSHTSSVNNITWSPSPADRL 803

QY 89 SINY 92

DB 804 ILNY 807

RESULT 12

A40701

tenascin-X precursor - human

C;Species: Homo sapiens (man)

C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 31-Dec-2004

C;Accession: A40701; A33725; C42175

R;Bristow, J.; Tee, M.K.; Gitelman, S.E.; Mellon, S.H.; Miller, W.L.

J. Cell Biol. 122, 265-278, 1993

A;Title: Tenascin-X: a novel extracellular matrix protein encoded by the human XB gene c

A;Reference number: A40701; MUID:93300909; PMID:7686164

A;Accession: A40701

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-3566 <BRI>

A;Cross-references: UNIPROT:P22105; UNIPROT:Q9UC11; UNIPARC:UPI0000174343; EMBL:X71937

R;Morel, Y.; Bristow, J.; Gitelman, S.E.; Miller, W.L.

Proc. Natl. Acad. Sci. U.S.A. 86, 6582-6586, 1989

A;Title: Transcript encoded on the opposite strand of the human steroid 21-hydroxylase/c

A;Reference number: A33725; MUID:69367293; PMID:2475872

A;Accession: A33725

A;Molecule type: mRNA

A;Residues: 2748-3199, 'V', 3201-3298, 'E', 3299-3314, 'G', 3316-3566 <MOR>

A;Cross-references: UNIPARC:UPI000016A98B; GB:M25813; NID:g183069; PIDN:AAA35984.1; PID:

R;Matsumoto, K.; Arai, M.; Ishihara, N.; Ando, A.; Inoko, H.; Ikemura, T.

Genomics 12, 485-491, 1992

A;Title: Cluster of fibronectin type III repeats found in the human major histocompatib

enascin.

A;Reference number: A42175; MUID:92217969; PMID:1373119

A;Accession: C42175

A;Molecule type: DNA

A;Residues: 1849-1936 <MAT>

A;Cross-references: UNIPARC:UPI000006F862

A;Experimental source: clone 3.9Kf3-1

A;Note: sequence extracted from NCBI backbone (NCBIP:95694)

C;Genetics:

A;Gene: GDB:TNXA; D6S103E; TNX; XA; XB

A;Cross-references: GDB:568487; OMIM:600261

A;Map position: 6p21.3-6p21.3

C;Superfamily: EGF homology; fibrinogen beta/gamma homology; fibronectin type III repeat

C;Keywords: extracellular matrix; glycoprotein

F;435-461/Domain: EGF homology <EGF>

F;748-828/Domain: fibronectin type III repeat homology <3F1>

F;829-856/Domain: fibronectin type III repeat homology #status atypical <3F2>

F;873-953/Domain: fibronectin type III repeat homology <3F3>

F;975-1055/Domain: fibronectin type III repeat homology <3F4>

F;1078-1158/Domain: fibronectin type III repeat homology <3F5>

F;1167-1247/Domain: fibronectin type III repeat homology <3F6>

F;1248-1317/Domain: fibronectin type III repeat homology #status atypical <3F7>

F;1323-1403/Domain: fibronectin type III repeat homology <3F8>

F;1412-1492/Domain: fibronectin type III repeat homology <3F9>

F;1510-1590/Domain: fibronectin type III repeat homology <3F10>

F;1618-1676/Domain: fibronectin type III repeat homology #status atypical <3F11>

F;1678-1749/Domain: fibronectin type III repeat homology #status atypical <3F12>

F;1751-1831/Domain: fibronectin type III repeat homology <3F13>

F;1849-1929/Domain: fibronectin type III repeat homology <3F14>

F;1955-2035/Domain: fibronectin type III repeat homology <3F15>

F;2061-2141/Domain: fibronectin type III repeat homology <3F16>

F;2167-2246/Domain: fibronectin type III repeat homology <3F17>

F;2274-2354/Domain: fibronectin type III repeat homology <3F18>

F;2382-2462/Domain: fibronectin type III repeat homology <3F19>

F;2488-2568/Domain: fibronectin type III repeat homology <3F20>

F;2584-2664/Domain: fibronectin type III repeat homology <3F21>

F;2677-2757/Domain: fibronectin type III repeat homology <3F22>

F;2771-2851/Domain: fibronectin type III repeat homology <3F23>

F;2878-2958/Domain: fibronectin type III repeat homology <3F24>

F;2977-3067/Domain: fibronectin type III repeat homology #status atypical <3F25>

F;3078-3159/Domain: fibronectin type III repeat homology <3F26>

F;3167-3247/Domain: fibronectin type III repeat homology <3F27>

F;3255-3334/Domain: fibronectin type III repeat homology <3F28>

F;3349-3557/Domain: fibrinogen beta/gamma homology <FBG>

Query Match 22.5%; Score 111; DB 1; Length 3566;

Best Local Similarity 31.9%; Pred. No. 0.012;

Matches 30; Conservative 18; Mismatches 40; Indels 6; Gaps 3;

QY 1 VSDVPRDLVVAATPTSLRSLWNRSGLQSYRYITVGETGNSPVQVFTVPPWASIIATIS 60

DB 748 VIDGPQDLRVVSTPTTLEGLWLRPQAEVDRFVVSV--VSADNQRVR-LEVPPTDGTLLT 805

QY 61 GLKPGVDYITVVAVTDKSDTYKYDDPISINRYT 94

DB 806 DLMFGVEYVTVTAERGRAVSY----PASVRANT 835

RESULT 13

S46216

leukocyte antigen-related protein precursor - rat

N;Alternate names: leukocyte common antigen homolog

N;Contains: protein-tyrosine-phosphatase (EC 3.1.3.48)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 20-Feb-1995 #sequence revision 20-Feb-1995 #text_change 09-Jul-2004

C;Accession: S46216; S23252; A41032; A33154

R;Zhang, W.R.; Hashimoto, N.; Ahmad, F.; Ding, W.; Goldstein, B.J.

Biochem. J. 302, 39-47, 1994

A;Title: Molecular cloning and expression of a unique receptor-like protein-tyrosine-pho

A;Reference number: S46216; MUID:94347119; PMID:8068021

A;Accession: S46216

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-1898 <ZHA>

A;Cross-references: UNIPROT:Q64604; UNIPARC:UPI000000E87A8; EMBL:U11586; NID:g205132; PID

R;Hashimoto, N.; Zhang, W.R.; Goldstein, B.J.

Biochem. J. 284, 569-576, 1992

A;Title: Insulin receptor and epidermal growth factor receptor dephosphorylation by three

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 23, 2006, 07:40:29 ; Search time 228 Seconds
(without alignments)
290.876 Million cell updates/sec

Title: US-09-688-566-81
Perfect score: 494
Sequence: 1 VSDVPRDLEVAATPTSLRI.....VTDKSDTYKYDDPISINRYT 94

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	361	73.1	787	2	Q5CZ99 HUMAN
2	361	73.1	1011	2	Q59G22 HUMAN
3	361	73.1	1034	2	Q6N084 HUMAN
4	361	73.1	1255	2	Q6NZS0 HUMAN
5	361	73.1	2146	2	Q68CX6 HUMAN
6	361	73.1	2217	2	Q585T2 HUMAN
7	361	73.1	2240	2	Q68DP8 HUMAN
8	361	73.1	2265	2	Q60FE4 HUMAN
9	361	73.1	2267	2	Q68DP9 HUMAN
10	361	73.1	2296	2	Q6N0A6 HUMAN
11	361	73.1	2351	2	Q59EH1 HUMAN
12	361	73.1	2357	2	Q68DH4 HUMAN
13	361	73.1	2386	1	FINC HUMAN
14	361	73.1	2444	2	Q6N0T5 HUMAN
15	361	73.1	2477	2	Q6MZU5 HUMAN
16	356	72.1	2193	2	Q6MZM7 HUMAN
17	354	71.7	2265	1	FINC BOVIN
18	333	67.4	2477	1	FINC MOUSE
19	333	67.4	2477	1	FINC RAT
20	311	63.0	1256	1	FINC CHICK
21	269	54.5	293	2	Q9XSG0 RABIT
22	264	53.4	1328	1	FINC FLEWA
23	262	53.0	2481	1	FINC XENLA
24	262	53.0	2481	2	Q6GQA5 XENLA
25	254	51.4	2383	2	Q4RNC4 TETNG
26	254	51.4	2475	2	Q501R6 XENOPUS
27	251	50.8	2478	2	Q93406 BRACHYDANIO
28	246	49.8	2408	2	Q6JANZ BRACHYDANIO
29	246	49.8	2500	2	Q58XP5 BRACHYDANIO
30	153	31.0	68	2	Q28692 ORYCTOLAGUS
31	130	26.3	522	1	FINC_HORSE

32	125	25.3	4006	2	O35452	MUS MUSCULU
33	125	25.3	4114	2	O54796	MUS MUSCULU
34	124	25.1	4135	2	O18977	BOS TAURUS
35	123	24.9	320	2	Q95KV4	BOS TAURUS
36	123	24.9	347	2	Q95KV5	BOS TAURUS
37	123	24.9	426	2	Q9NPK8	HOMO SAPIEN
38	123	24.9	522	1	FINC CANFA	
39	123	24.9	1350	2	Q7T3T6	BRACHYDANIO
40	123	24.9	4222	2	Q5ST74	HOMO SAPIEN
41	123	24.9	4222	2	Q5SQD3	HOMO SAPIEN
42	123	24.9	4288	2	Q9NPK9	HOMO SAPIEN
43	123	24.9	4289	1	TENX HUMAN	
44	122	24.7	354	2	Q9UQ56	HOMO SAPIEN
45	122	24.7	379	2	O95617	HOMO SAPIEN

ALIGNMENTS

RESULT 1
Q5CZ99_HUMAN PRELIMINARY; PRT; 787 AA.
AC Q5CZ99;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE Hypothetical protein DKFZp686I1370 (Fragment).
GN Name=DKFZp686I1370;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Endometrium carcinoma cell line;
RG The German cDNA Consortium;
RA Ansorge W., Krieger S., Regiert T., Rittmuller C., Schwager B.,
RA Mewes H.W., Weil B., Amid C., Oeinger A., Fobo G., Han M., Wiemann S.;
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR936623; CA156766.1; -, mRNA.
DR InterPro; IPR002086; Aldehyd dehydrog.
DR InterPro; IPR003961; FN_III subd.
DR InterPro; IPR003961; FN_III.
DR Pfam; PF00041; fn3_8.
DR PRINTS; PR00014; FNTYPEIII.
DR SMART; SM00060; FN3; 8.
DR PROSITE; PS00687; ALDEHYDE DEHYDR_GLU; UNKNOWN_1.
DR PROSITE; PS00853; FN3; 9.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 787 AA; 85622 MW; 5B49003169158ADD CRC64;

Query Match 73.1%; Score 361; DB 2; Length 787;

Best Local Similarity 77.7%; Pred. No. 2.4e-30;

Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

Qy 1 VSDVPRDLEVAATPTSLRI...VTDKSDTYKYDDPISINRYT 94

Db 237 VSDVPRDLEVAATPTSLRI...VTDKSDTYKYDDPISINRYT 330

Qy 61 GLKPGVDYTTIVAVTDKSDTYKYDDPISINRYT 94

Db 297 GLKPGVDYTTIVAVTDKSDTYKYDDPISINRYT 330

RESULT 2

Q59G22_HUMAN PRELIMINARY; PRT; 1011 AA.

AC Q59G22;

DT 10-MAY-2005 (TrEMBLrel. 30, Created)

DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)

DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)


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AC Q68CX6;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein DKFZp686O13149.
GN Name=DKFZp686O13149;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Colon endoethel;
RG The German cDNA Consortium;
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR749666; CAH18457.1; -; mRNA.
DR SMR; Q68CX6; 1-258, 349-442, 441-709, 1061-1331.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0016491; P:oxidoreductase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR02086; Aldehyd dehydrog.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR000083; Fibrinctnl.
DR InterPro; IPR003962; FNIII subd.
DR InterPro; IPR003961; FN_III.
DR Pfam; PF00039; fnl; 6.
DR Pfam; PF00041; fn3; 18.
DR PRINTS; PR00012; FNTYPEII.
DR PRINTS; PR00014; FNTYPEIII.
DR SMART; SM00058; FN1; 6.
DR SMART; SM00060; FN3; 18.
DR PROSITE; PS00687; ALDEHYDE DEHYDR_GLU; 2.
DR PROSITE; PS00022; EGF_1; 2.
DR PROSITE; PS01253; FIBRONECTIN_1; 6.
DR PROSITE; PS05853; FN3; 18.
KW Hypothetical protein.
SQ SEQUENCE 2146 AA; 235425 MW; D526A8D713C571DE CRC64;

Query Match 73.1%; Score 361; DB 2; Length 2146;
Best Local Similarity 77.7%; Pred. No. 8e-30;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

Qy 1 VSDVPRDLEVAATPTSLRSLNSGLOSRYRITYTGTGNSPVQSFVPPWASIIATIS 60
Db 165 VSDVPRDLEVAATPTSLRSLNSGLOSRYRITYTGTGNSPVQSFVPPWASIIATIS 224

Qy 61 GLKPGVDYTTTVAATDKSTYKYDDPISINRYT 94
Db 225 GLKPGVDYTTTVAATGRGDSPASSKPFISINRYT 258

RESULT 6
Q585T2 HUMAN
ID Q585T2 HUMAN PRELIMINARY; PRT; 2217 AA.
AC Q585T2;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein FN1 (Fragment).
GN Name=FN1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Waterston R.H.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [2]

RP NUCLEOTIDE SEQUENCE.
RA Waterston R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Wilson R.K.;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC012462; AAX76513.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON_TER 2217
SQ SEQUENCE 2217 AA; 243438 MW; FAF1D07FBB6C44E5 CRC64;

Query Match 73.1%; Score 361; DB 2; Length 2217;
Best Local Similarity 77.7%; Pred. No. 8.3e-30;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

Qy 1 VSDVPRDLEVAATPTSLRSLNSGLOSRYRITYTGTGNSPVQSFVPPWASIIATIS 60
Db 1447 VSDVPRDLEVAATPTSLRSLNSGLOSRYRITYTGTGNSPVQSFVPPWASIIATIS 1506

Qy 61 GLKPGVDYTTTVAATDKSTYKYDDPISINRYT 94
Db 1507 GLKPGVDYTTTVAATGRGDSPASSKPFISINRYT 1540

RESULT 7
Q68DP8 HUMAN
ID Q68DP8 HUMAN PRELIMINARY; PRT; 2240 AA.
AC Q68DP8;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein DKFZp686H0342.
GN Name=DKFZp686H0342;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Amnygdala;
RG The German cDNA Consortium;
RA Ottenwaelder B., Obermaier B., Deutschenbaur S., Schaipp A.,
RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR749317; CAH18172.1; -; mRNA.
DR SMR; Q68DP8; 48-140, 305-464, 609-701, 1173-1540, 1633-1901.
DR Ensembl; ENSG00000115414; Homo sapiens.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0016491; P:oxidoreductase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR02086; Aldehyd dehydrog.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR000083; Fibrinctnl.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR000562; FN_type2_col_bd.
DR InterPro; IPR003962; FNIII_subd.
DR Pfam; PF00039; fnl; 12.
DR Pfam; PF00040; fn2; 2.
DR Pfam; PF00041; fn3; 15.
DR PRINTS; PR00012; FNTYPEI.
DR PRINTS; PR00013; FNTYPEII.
DR PRINTS; PR00014; FNTYPEIII.
DR PRODOM; PD000995; FN_Type_II; 2.
DR SMART; SM00058; FN1; 12.
DR SMART; SM00059; FN2; 2.
DR SMART; SM00060; FN3; 15.
DR PROSITE; PS00687; ALDEHYDE DEHYDR_GLU; 1.
DR PROSITE; PS00022; EGF_1; 2.
DR PROSITE; PS01253; FN1_1; 10.
DR PROSITE; PS01253; FN1_2; 10.
DR PROSITE; PS01091; FN1_2; 10.
DR PROSITE; PS00023; FN2_1; 2.
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Qy Db

DE Hypothetical protein DKF2p686M04163.
GS Name=DKF2p686M04163;
ON Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=uterus endothel;
RG The German cDNA Consortium;
RA Bloecher H., Boeher M., Brandt P., Mewes H.W., Weil B., Amid C.,
RA Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL: BX640608; CA845714.1; -; mRNA.
DR GO: 0005576; C:extracellular region; IEA.
DR InterPro; IPR02086; ALDEHYD DEHYDR.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR00083; Fibrinctnl.
DR InterPro; IPR003962; FNIII subd.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR00562; FN_Type_II.
DR Pfam; PF00039; fn1; 12.
DR Pfam; PF00040; fn2; 2.
DR Pfam; PF00041; fn3; 15.
DR PRINTS; PR00012; FNTYPEI.
DR PRINTS; PR00013; FNTYPEII.
DR PRINTS; PR00014; FNTYPEIII.
DR ProDom; PD000995; FN_Type_II; 2.
DR SMART; SM00058; FN1; 2.
DR SMART; SM00059; FN2; 2.
DR SMART; SM00060; FN3; 15.
DR PROSITE; PS00687; ALDEHYDE DEHYDR_GLU; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_2.
DR PROSITE; PS01253; FIBRONECTIN_1; 12.
DR PROSITE; PS00023; FIBRONECTIN_2; 2.
DR PROSITE; PS00853; FN3; 15.
KW Hypothetical protein.
SQ SEQUENCE 2296 AA; 252761 MW; 9AB2D723CC0CED70 CRC64;

Query Match 73.1%; Score 361; DB 2; Length 2296;
Best Local Similarity 77.7%; Pred. No. 8.6e-30;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

QY 1 VSDVPRDLEVVAAATPTSLISWNRSGLQSYRYRITYGTGNSPVQSFYPPWASIASIS 60
DB 1447 VSDVPRDLEVVAAATPTSLISWNRSGLQSYRYRITYGTGNSPVQSFYPPWASIASIS 1506

QY 61 GLKPGVDYTTIVAVTDKSDTYKYDDPISINRYT 94
DB 1507 GLKPGVDYTTIVAVTGRGDSPPASSKPIISINRYT 1540

RESULT 11
Q59EHL_HUMAN PRELIMINARY; PRT; 2351 AA.
AC Q59EHL_HUMAN
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE Fibronectin 1 variant (fragment).
GN Name=Fibronectin 1 variant;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Aorta endothelial cell;
RA Totoki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama S.,
RA Ohara O., Nagase T., Kikuno F.R.;
RT "None Title."

DE Hypothetical protein DKF2p686M04163.
GS Name=DKF2p686M04163;
ON Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=uterus endothel;
RG The German cDNA Consortium;
RA Bloecher H., Boeher M., Brandt P., Mewes H.W., Weil B., Amid C.,
RA Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL: BX640608; CA845714.1; -; mRNA.
DR GO: 0005576; C:extracellular region; IEA.
DR InterPro; IPR02086; ALDEHYD DEHYDR.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR00083; Fibrinctnl.
DR InterPro; IPR003962; FNIII subd.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR00562; FN_Type_II.
DR Pfam; PF00039; fn1; 12.
DR Pfam; PF00040; fn2; 2.
DR Pfam; PF00041; fn3; 15.
DR PRINTS; PR00012; FNTYPEI.
DR PRINTS; PR00013; FNTYPEII.
DR PRINTS; PR00014; FNTYPEIII.
DR ProDom; PD000995; FN_Type_II; 2.
DR SMART; SM00058; FN1; 2.
DR SMART; SM00059; FN2; 2.
DR SMART; SM00060; FN3; 15.
DR PROSITE; PS00687; ALDEHYDE DEHYDR_GLU; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_2.
DR PROSITE; PS01253; FIBRONECTIN_1; 12.
DR PROSITE; PS00023; FIBRONECTIN_2; 2.
DR PROSITE; PS00853; FN3; 15.
KW Hypothetical protein.
SQ SEQUENCE 2296 AA; 252761 MW; 9AB2D723CC0CED70 CRC64;

Query Match 73.1%; Score 361; DB 2; Length 2296;
Best Local Similarity 77.7%; Pred. No. 8.6e-30;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

QY 1 VSDVPRDLEVVAAATPTSLISWNRSGLQSYRYRITYGTGNSPVQSFYPPWASIASIS 60
DB 1447 VSDVPRDLEVVAAATPTSLISWNRSGLQSYRYRITYGTGNSPVQSFYPPWASIASIS 1506

QY 61 GLKPGVDYTTIVAVTDKSDTYKYDDPISINRYT 94
DB 1507 GLKPGVDYTTIVAVTGRGDSPPASSKPIISINRYT 1540

RESULT 11
Q59EHL_HUMAN PRELIMINARY; PRT; 2351 AA.
AC Q59EHL_HUMAN
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE Fibronectin 1 variant (fragment).
GN Name=Fibronectin 1 variant;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Aorta endothelial cell;
RA Totoki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama S.,
RA Ohara O., Nagase T., Kikuno F.R.;
RT "None Title."

RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB209840; BAD93077.1; -; mRNA.
FT NON_TER 1 1
SQ SEQUENCE 2351 AA; 258611 MW; 67149C626199075E CRC64;

Query Match 73.1%; Score 361; DB 2; Length 2351;
Best Local Similarity 77.7%; Pred. No. 8.9e-30;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

QY 1 VSDVPRDLEVVAAATPTSLISWNRSGLQSYRYRITYGTGNSPVQSFYPPWASIASIS 60
DB 1533 VSDVPRDLEVVAAATPTSLISWNRSGLQSYRYRITYGTGNSPVQSFYPPWASIASIS 1592

QY 61 GLKPGVDYTTIVAVTDKSDTYKYDDPISINRYT 94
DB 1593 GLKPGVDYTTIVAVTGRGDSPPASSKPIISINRYT 1626

RESULT 12
Q68DT4_HUMAN PRELIMINARY; PRT; 2357 AA.
AC Q68DT4_HUMAN
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein DKF2p686F10164.
GN Name=DKF2p686F10164;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=uterus endothel;
RG The German cDNA Consortium;
RA Koehrer K., Beyer A., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: CR749281; CAH18136.1; -; mRNA.
DR GO: 0005576; C:extracellular region; IEA.
DR GO: 0016491; F:oxidoreductase activity; IEA.
DR GO: 0008152; P:metabolism; IEA.
DR InterPro; IPR002086; ALDEHYD DEHYDR.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR00083; Fibrinctnl.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR00562; FN_Type_II; 2.
DR Pfam; PF00039; fn1; 12.
DR Pfam; PF00040; fn2; 2.
DR Pfam; PF00041; fn3; 15.
DR PRINTS; PR00012; FNTYPEI.
DR PRINTS; PR00013; FNTYPEII.
DR PRINTS; PR00014; FNTYPEIII.
DR ProDom; PD000995; FN_Type_II; 2.
DR SMART; SM00058; FN1; 12.
DR SMART; SM00059; FN2; 2.
DR SMART; SM00060; FN3; 15.
DR PROSITE; PS00687; ALDEHYDE DEHYDR_GLU; 1.
DR PROSITE; PS00022; EGF_1; 2.
DR PROSITE; PS01253; FN1_1; 12.
DR PROSITE; PS01091; FN1_2; 12.
DR PROSITE; PS00023; FN2_1; 2.
DR PROSITE; PS1092; FN2_2; 2.
DR PROSITE; PS00853; FN3; 15.
KW Hypothetical protein; Repeat.
SQ SEQUENCE 2357 AA; 259092 MW; BEAE3990E27E532A CRC64;

Query Match 73.1%; Score 361; DB 2; Length 2357;
Best Local Similarity 77.7%; Pred. No. 8.9e-30;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

[18]
RN NUCLEOTIDE SEQUENCE OF 1712-1739.
RP MEDLINE=87026578; PubMed=3021206;
RA Sekiguchi K., Klos A.M., Kurachi K., Yoshitake S., Hakomori S.;
RT "Human liver fibronectin complementary DNAs: identification of two
RT different messenger RNAs possibly encoding the alpha and beta subunits
RT of plasma fibronectin.";
RL Biochemistry 25:4936-4941(1986).
RN [19]
RN NUCLEOTIDE SEQUENCE OF 1788-2386 (ISOFORMS 4; 5 AND 6).
RP TISSUE=Cartilage;
RC MEDLINE=22126816; PubMed=12127832; DOI=10.1053/joca.2002.0792;
RA Parker A.E., Boutell J., Carr A., Maciewicz R.A.;
RT "Novel cartilage-specific variants of fibronectin.";
RL Osteoarthritis Cartilage 10:528-534(2002).
RN [20]
RN NUCLEOTIDE SEQUENCE OF 1948-2067.
RP MEDLINE=85231203; PubMed=2989004; DOI=10.1016/0014-5793(85)81333-8;
RA Umezawa K., Kornblitt A.R., Baralle F.E.;
RT "Isolation and characterization of cDNA clones for human liver
RT fibronectin.";
RL FEBS Lett. 186:31-34(1985).
RN [21]
RN NUCLEOTIDE SEQUENCE OF 1992-2147.
RP MEDLINE=87030929; PubMed=3770201; DOI=10.1016/0014-5793(86)81506-X;
RA Vibe-Pedersen K., Magnusson S., Baralle F.E.;
RT "Donor and acceptor splice signals within an exon of the human
RT fibronectin gene: a new type of differential splicing.";
RL FEBS Lett. 207:287-291(1986).
RN [22]
RN PROTEIN SEQUENCE OF 2071-2356 (ISOFORM 3).
RP MEDLINE=85261459; PubMed=4019516;
RA Garcia-Pardo A., Pearlstein E., Frangione B.;
RT "Primary structure of human plasma fibronectin. Characterization of a
RT 31,000-dalton fragment from the COOH-terminal region containing a free
RT sulfhydryl group and a fibrin-binding site.";
RL J. Biol. Chem. 260:10320-10325(1985).
RN [23]
RN NUCLEOTIDE SEQUENCE OF 2291-2386.
RP PubMed=6304699;
RA Kornblitt A.R., Vibe-Pedersen K., Baralle F.E.;
RT "Isolation and characterization of cDNA clones for human and bovine
RT fibronectins.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:3218-3222(1983).
RN [24]
RN PROTEIN SEQUENCE OF 32-290.
RP MEDLINE=84032463; PubMed=6630202;
RA Garcia-Pardo A., Pearlstein E., Frangione B.;
RT "Primary structure of human plasma fibronectin. The 29,000-dalton NH2-
RT terminal domain.";
RL J. Biol. Chem. 258:12670-12674(1983).
RN [25]
RN PROTEIN SEQUENCE OF 309-608, AND COLLAGEN-BINDING.
RP MEDLINE=87080265; PubMed=3024962;
RA Owens R.J., Baralle F.E.;
RT "Mapping the collagen-binding site of human fibronectin by expression
RT in Escherichia coli.";
RL EMBO J. 5:2825-2830(1986).
RN [26]
RN SULFATION.
RP MEDLINE=86042625; PubMed=2414772;
RA Liu M.C., Yu S., Sy J., Redman C.M., Lipmann F.;
RT "Tyrosine sulfation of proteins from the human hepatoma cell line
RT HepG2.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:7160-7164(1985).
RN
Query Match 73.1%; Score 361; DB 1; Length 2386;
Best Local Similarity 77.7%; Pred. No. 9e-30;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;
Qy 1 VSDVPRDLVVAATPTSLISWDAFVTVYRITYTGSGNSPVQEFVPPWASIAIIS 60
Db 1447 VSDVPRDLVVAATPTSLISWDAFVTVYRITYTGSGNSPVQEFVPPWASIAIIS 1506

Qy 61 GLKPGVDYTTIVAVTDKSDTYKYDDPISINYRT 94
Db 1507 GLKPGVDYTTIVAVTGRGDSPASSKPFISINYRT 1540
RESULT 14
Q6N025_HUMAN
ID Q6N025_HUMAN PRELIMINARY; PRT; 2444 AA.
AC Q6N025; 2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686M2451 (Fragment).
GN Name=DKFZp686M2451;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Theria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Human endometrium carcinoma cell line;
RA The German Human cDNA Consortium;
RA Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX40731; CA545847.1; -, mRNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR InterPro; IPR002086; Aldehyd dehydrog.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR000083; Fibrinctnl.
DR InterPro; IPR003962; FcIII subd.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR000562; FN_type_II.
DR Pfam; PF00039; fn1; 12.
DR Pfam; PF00040; fn2; 2.
DR Pfam; PF00041; fn3; 16.
DR PRINTS; PR00012; FNTYPEI.
DR PRINTS; PR00014; FNTYPEII.
DR PRINTS; PR00014; FNTYPEIII.
DR ProDom; PD000995; FN_type_II; 2.
DR SMART; SM00058; FN1; 12.
DR SMART; SM00059; FN2; 2.
DR SMART; SM00060; FN3; 16.
DR PROSITE; PS00687; ALDEHYDE DEHYD GLU; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_2.
DR PROSITE; PS01253; FIBRONECTIN_1; 12.
DR PROSITE; PS00023; FIBRONECTIN_2; 2.
DR PROSITE; PS00853; FN3; 16.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 2444 AA; 268676 MW; 71C5B8C56A84C7BC CRC64;
Query Match 73.1%; Score 361; DB 2; Length 2444;
Best Local Similarity 77.7%; Pred. No. 9.3e-30;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;
Qy 1 VSDVPRDLVVAATPTSLISWDAFVTVYRITYTGSGNSPVQEFVPPWASIAIIS 60
Db 1536 VSDVPRDLVVAATPTSLISWDAFVTVYRITYTGSGNSPVQEFVPPWASIAIIS 1595
Qy 61 GLKPGVDYTTIVAVTDKSDTYKYDDPISINYRT 94
Db 1596 GLKPGVDYTTIVAVTGRGDSPASSKPFISINYRT 1629
RESULT 15
Q6MZU5_HUMAN
ID Q6MZU5_HUMAN PRELIMINARY; PRT; 2477 AA.
AC Q6MZU5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT	05-JUL-2004	(TrEMBL)rel. 27, Last annotation update)	
DE	Hypothetical protein DKFZp686O1166.		
GN	Name=DKFZp686O1166;		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;		
OC	Homo.		
NCBI_TaxID=9606;			
11			
RP	NUCLEOTIDE SEQUENCE		
RC	TISSUE=Endometrium carcinoma cell line;		
RG	The German cDNA Consortium;		
RA	Bloecker H., Boecher M., Brandt P., Mewes H.W., Weil B., Amid C.,		
RS	Osanger A., Fobo G., Han M., Wiemann S.;		
RL	Submitted (PEB-2005) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; BX40875; CA945932.1; ; mRNA.		
DR	GO; GO:0005576; C:extracellular region; IEA.		
DR	InterPro; IPR002086; Aldehyde dehydrog.		
DR	InterPro; IPR006209; EGF like.		
DR	InterPro; IPR000083; Fibrinctnl.		
DR	InterPro; IPR003962; FNIII subd.		
DR	InterPro; IPR003961; FN_III.		
DR	InterPro; IPR000562; FN_Type_II.		
DR	Pfam; PF00039; fn1; 12.		
DR	Pfam; PF00040; fn2; 2.		
DR	Pfam; PF00041; fn3; 17.		
DR	PRINTS; PR00012; FNTYPEI.		
DR	PRINTS; PR00013; FNTYPEII.		
DR	PRINTS; PR00014; FNTYPEIII.		
DR	ProDom; PD000995; FN_Type_II; 2.		
DR	SMART; SM00058; FN1; 12.		
DR	SMART; SM00059; FN2; 2.		
DR	SMART; SM00060; FN3; 17.		
DR	PROSITE; PS00687; ALDEHYDE DEHYD GLU; UNKNOWN 1.		
DR	PROSITE; PS00022; EGF_1; UNKNOWN 2.		
DR	PROSITE; PS01253; FIBRONECTIN_1; 12.		
DR	PROSITE; PS00023; FIBRONECTIN_2; 2.		
DR	PROSITE; PS00853; FN3; 17.		
KW	Hypothetical protein.		
SEQ	SEQUENCE 2477 AA; 272335 MW; D358D85C6B18207C CRC64;		
	Query Match	73.1%; Score 361; DB 2; Length 2477;	
	Best Local Similarity	77.7%; Pred. No. 9.5e-30;	
	Matches	73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;	
Qy	1	VSDVPRDLVVAAPTPTSLRLISWNRSGLQSRYYRITYGETGNSPVQFTVPPWIASIATIS 60	
Db	1538	VSDVPRDLVVAAPTPTSLILISWDAPAVTVYRITYGETGNSPVQFTVPGSKSTATIS 1597	
Qy	61	GLKPGVDYTTTVAVTGKSDTYKYDDDISINRYT 94	
Db	1598	GLKPGVDYTTTVAVTGRTGDSPASSKDISINRYT 1631	

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OM protein - protein search, using sw model

Run on: February 23, 2006, 07:40:25 ; Search time 186 Seconds
(without alignments)
222.052 Million cell updates/sec

Title: US-09-688-566-81

Perfect score: 494

Sequence: 1 VSDVPRDLEVAATPTSLRI.....VTDKSTYKYDDPISINVRT 94

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq 21:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1980s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2000s:*
- 5: Geneseqp2000s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*
- 9: Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	494	100.0	94	5 ABB78921	Abb78921 Tumour ne
3	489	99.0	94	5 ABB78939	Abb78939 Tumour ne
4	489	99.0	94	5 ABB78919	Abb78919 Tumour ne
5	489	99.0	94	5 ABB78920	Abb78920 Tumour ne
6	488	98.8	94	5 ABB78911	Abb78911 Tumour ne
7	486	98.4	94	5 ABB78915	Abb78915 Tumour ne
8	484	98.0	94	5 ABB78940	Abb78940 Tumour ne
9	484	98.0	94	5 ABB78912	Abb78912 Tumour ne
10	483	97.8	94	5 ABB78916	Abb78916 Tumour ne
11	483	97.8	94	5 ABB78918	Abb78918 Tumour ne
12	481	97.4	94	5 ABB78899	Abb78899 Tumour ne
13	478	96.8	94	5 ABB78917	Abb78917 Tumour ne
14	463	93.7	94	5 ABB78922	Abb78922 Tumour ne
15	446	90.3	94	5 ABB78923	Abb78923 Tumour ne
16	443	89.7	94	5 ABB78949	Abb78949 Tumour ne
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19	437	88.5	93	5 ABB78868	Abb78868 Tumour ne
20	431	87.2	94	5 ABB78872	Abb78872 Tumour ne
21	419	84.8	94	5 ABB78942	Abb78942 Tumour ne
22	417	84.4	94	5 ABB78870	Abb78870 Tumour ne
23	416	84.2	94	5 ABB78900	Abb78900 Tumour ne
24	415	84.0	94	5 ABB78871	Abb78871 Tumour ne

25	406	82.2	94	5 ABB78895	Abb78895 Tumour ne
26	402	81.4	94	5 ABB78941	Abb78941 Tumour ne
27	397	80.4	94	5 ABB78901	Abb78901 Tumour ne
28	395	80.0	76	5 ABB78897	Abb78897 Tumour ne
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30	392	79.4	94	5 ABB78879	Abb78879 Tumour ne
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32	390	78.9	94	5 ABB78954	Abb78954 Tumour ne
33	390	78.9	94	5 ABB78910	Abb78910 Tumour ne
34	389	78.7	94	5 ABB78881	Abb78881 Tumour ne
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39	385	77.9	94	5 ABB78864	Abb78864 Tumour ne
40	384	77.7	94	5 ABB78867	Abb78867 Tumour ne
41	384	77.7	94	5 ABB78904	Abb78904 Tumour ne
42	382.5	77.4	93	5 ABB78878	Abb78878 Tumour ne
43	382	77.3	94	5 ABB78877	Abb78877 Tumour ne
44	380	76.9	94	5 ABB78866	Abb78866 Tumour ne
45	374	75.7	94	5 ABB78929	Abb78929 Tumour ne

ALIGNMENTS

RESULT 1
ABB78898
ID ABB78898 standard; peptide; 94 AA.
XX
AC ABB78898;
XX
DT 30-JUL-2002 (first entry)
XX
DE Tumour necrosis factor-alpha binding amino acid sequence T10.06.
DE
KW Protein scaffold; antibody; binding protein; immunoglobulin;
KW tumour necrosis factor alpha; TNF-alpha; protein framework.
XX
XX Homo sapiens.
OS Synthetic.
OS
PN WO200232925-A2.
XX
PD 25-APR-2002.
XX
PF 16-OCT-2001; 2001WO-US032233.
XX
PR 16-OCT-2000; 2000US-00688566.
XX
XX (PHYL-) PHYLLOS INC.
XX
XX Lipovsek D, Wagner RW, Kuimelis RG;
XX WPI; 2002-444238/47.
XX
PT New non-antibody proteins having an immunoglobulin fold, useful in
PT research, therapeutic or diagnostic fields, particularly as scaffolds for
PT designing proteins with specific properties, e.g. for binding any antigen
of interest.
XX
XX Claim 47; Fig 25; 94pp; English.
XX
CC The present invention describes a non-antibody protein, comprising a
CC domain having an immunoglobulin-like fold, derived from a reference
CC protein having a mutated amino acid sequence, where the non-antibody
CC protein binds with a Kd at least as tight as 10 nM to a compound that is
CC not bound as tightly by the reference protein. The non-antibody protein
CC is useful as scaffolds for selecting or designing a protein framework
CC with specific and favourable properties, e.g. for binding any antigen of
CC interest, or for destroying or inactivating antibody molecules. The non-
CC antibody protein is also useful in all areas where antibodies are used,
CC e.g. research, therapeutic or diagnostic fields, and for screening novel

CC binding proteins useful in the above-mentioned fields. The present
CC proteins have thermodynamic properties superior to those of natural
CC antibodies, and can be evolved rapidly in vitro. The present proteins or
CC antibody mimics exhibit improved biophysical properties, such as
CC stability under reducing conditions and solubility at high
CC concentrations. In addition, these molecules are readily expressed and
CC folded in prokaryotic systems (e.g. Escherichia coli), in eukaryotic
CC systems (e.g. yeast), or in in vitro translation systems (e.g. rabbit
CC reticulocyte lysate system). Furthermore, these proteins are extremely
CC amenable to affinity maturation techniques involving multiple cycles of
CC selection, e.g. in vitro selection using RNA-protein fusion technology,
CC phage display or yeast display systems. The present sequence is used in
CC the exemplification of the present invention

XX
SQ Sequence 94 AA;

Query Match 100.0%; Score 494; DB 5; Length 94;
Best Local Similarity 100.0%; Pred. No. 1.2e-49;
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSDVPRDLEVVAATPTSRLLISWNRSGLSQRYRYRITYGETGNSPVQEFVPPWASITATIS 60
Db |||||
QY 61 GLKPGVDYITTVYAVTDKSDTYKYDDPISINVRT 94
Db |||||

RESULT 2
ABB78921

ID ABB78921 standard; peptide; 94 AA.
XX
AC ABB78921;
DT 30-JUL-2002 (first entry)
XX
DE Tumour necrosis factor-alpha binding amino acid sequence T14.26.
XX
KW Protein scaffold; antibody; binding protein; immunoglobulin;
KW tumour necrosis factor alpha; TNF-alpha; protein framework.
XX
OS Homo sapiens.
OS Synthetic.
XX WO200232925-A2.
XX
XX 25-APR-2002.
XX
XX 16-OCT-2001; 2001WO-US032233.
XX
XX 16-OCT-2000; 2000US-00688566.
XX
XX (PHYL-) PHYLLOS INC.
XX
PI Lipovsek D, Wagner RW, Kuimelis RG;
XX WPI; 2002-444238/47.
XX
XX New non-antibody proteins having an immunoglobulin fold, useful in
PT research, therapeutic or diagnostic fields, particularly as scaffolds for
PT designing proteins with specific properties, e.g. for binding any antigen
PT of interest.
XX
XX Claim 47; Fig 25; 94pp; English.
XX
XX The present invention describes a non-antibody protein, comprising a
CC domain having an immunoglobulin-like fold, derived from a reference
CC protein having a mutated amino acid sequence, where the non-antibody
CC protein binds with a Kd at least as tight as 10 nM to a compound that is
CC not bound as tightly by the reference protein. The non-antibody protein
CC is useful as scaffolds for selecting or designing a protein framework
CC with specific and favourable properties, e.g. for binding any antigen of

CC interest, or for destroying or inactivating antibody molecules. The non-
CC antibody protein is also useful in all areas where antibodies are used,
CC e.g. research, therapeutic or diagnostic fields, and for screening novel
CC binding proteins useful in the above-mentioned fields. The present
CC proteins have thermodynamic properties superior to those of natural
CC antibodies, and can be evolved rapidly in vitro. The present proteins or
CC antibody mimics exhibit improved biophysical properties, such as
CC stability under reducing conditions and solubility at high
CC concentrations. In addition, these molecules are readily expressed and
CC folded in prokaryotic systems (e.g. Escherichia coli), in eukaryotic
CC systems (e.g. yeast), or in in vitro translation systems (e.g. rabbit
CC reticulocyte lysate system). Furthermore, these proteins are extremely
CC amenable to affinity maturation techniques involving multiple cycles of
CC selection, e.g. in vitro selection using RNA-protein fusion technology,
CC phage display or yeast display systems. The present sequence is used in
CC the exemplification of the present invention

XX
SQ Sequence 94 AA;

Query Match 100.0%; Score 494; DB 5; Length 94;
Best Local Similarity 100.0%; Pred. No. 1.2e-49;
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSDVPRDLEVVAATPTSRLLISWNRSGLSQRYRYRITYGETGNSPVQEFVPPWASITATIS 60
Db |||||
QY 61 GLKPGVDYITTVYAVTDKSDTYKYDDPISINVRT 94
Db |||||

RESULT 3
ABB78939

ID ABB78939 standard; peptide; 94 AA.
XX
AC ABB78939;
DT 30-JUL-2002 (first entry)
XX
DE Tumour necrosis factor-alpha binding amino acid sequence M12.01.
XX
KW Protein scaffold; antibody; binding protein; immunoglobulin;
KW tumour necrosis factor alpha; TNF-alpha; protein framework.
XX
OS Homo sapiens.
OS Synthetic.
XX WO200232925-A2.
XX
XX 25-APR-2002.
XX
XX 16-OCT-2001; 2001WO-US032233.
XX
XX 16-OCT-2000; 2000US-00688566.
XX
XX (PHYL-) PHYLLOS INC.
XX
PI Lipovsek D, Wagner RW, Kuimelis RG;
XX WPI; 2002-444238/47.
XX
XX New non-antibody proteins having an immunoglobulin fold, useful in
PT research, therapeutic or diagnostic fields, particularly as scaffolds for
PT designing proteins with specific properties, e.g. for binding any antigen
PT of interest.
XX
XX Claim 47; Fig 25; 94pp; English.
XX
XX The present invention describes a non-antibody protein, comprising a
CC domain having an immunoglobulin-like fold, derived from a reference
CC protein having a mutated amino acid sequence, where the non-antibody
CC protein binds with a Kd at least as tight as 10 nM to a compound that is
CC not bound as tightly by the reference protein. The non-antibody protein
CC is useful as scaffolds for selecting or designing a protein framework
CC with specific and favourable properties, e.g. for binding any antigen of

CC not bound as tightly by the reference protein. The non-antibody protein
 CC is useful as scaffolds for selecting or designing a protein framework
 CC with specific and favourable properties, e.g. for binding any antigen of
 CC interest, or for destroying or inactivating antibody molecules. The non-
 CC antibody protein is also useful in all areas where antibodies are used,
 CC e.g. research, therapeutic or diagnostic fields, and for screening novel
 CC binding proteins useful in the above-mentioned fields. The present
 CC proteins have thermodynamic properties superior to those of natural
 CC antibodies, and can be evolved rapidly in vitro. The present proteins or
 CC antibody mimics exhibit improved biophysical properties, such as
 CC stability under reducing conditions and solubility at high
 CC concentrations. In addition, these molecules are readily expressed and
 CC folded in prokaryotic systems (e.g. *Escherichia coli*), in eukaryotic
 CC systems (e.g. yeast), or in in vitro translation systems (e.g. rabbit
 CC reticulocyte lysate system). Furthermore, these proteins are extremely
 CC amenable to affinity maturation techniques involving multiple cycles of
 CC selection, e.g. in vitro selection using RNA-protein fusion technology,
 CC phage display or yeast display systems. The present sequence is used in
 CC the exemplification of the present invention

XX SQ Sequence 94 AA;

Query Match 99.0%; Score 489; DB 5; Length 94;
 Best Local Similarity 97.9%; Pred. No. 4.4e-49;
 Matches 92; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSDVPRDLEVVAAATPTSRLLISWNRSGLQSRYYRITYTGTCGNSPVQEFVPPWASIAIS 60
 DB 1 VSDVPRDLEVVAAATPTSRLLISWNRSGLQSRYYRITYTGTCGNSPVQEFVPPWASIAIS 60
 QY 61 GLKPGVDYITTVAVTDKSDTYKYDDPISINRYT 94
 DB 61 GLKPGVDYITTVAVTDKSDTYKYDDPISINRYT 94

RESULT 4

ABB78919
 ID ABB78919 standard; peptide; 94 AA.

XX AC ABB78919;

DT 30-JUL-2002 (first entry)

XX Tumour necrosis factor-alpha binding amino acid sequence T14.14.

XX Protein scaffold; antibody; binding protein; immunoglobulin;
 KW tumour necrosis factor alpha; TNF-alpha; protein framework.

XX Homo sapiens.

OS Synthetic.

PN WO200232925-A2.

XX 25-APR-2002.

XX 16-OCT-2001; 2001WO-US032233.

XX 16-OCT-2000; 2000US-00688566.

XX (PHYL-) PHYLLOS INC.

XX Lipovsek D, Wagner RW, Kuimelis RG;

XX WPI; 2002-444238/47.

XX New non-antibody proteins having an immunoglobulin fold, useful in
 PT research, therapeutic or diagnostic fields, particularly as scaffolds for
 PT designing proteins with specific properties, e.g. for binding any antigen
 PT of interest.

XX Claim 47; Fig 25; 94pp; English.

XX The present invention describes a non-antibody protein, comprising a

CC domain having an immunoglobulin-like fold, derived from a reference
 CC protein having a mutated amino acid sequence, where the non-antibody
 CC protein binds with a Kd at least as tight as 10 nM to a compound that is
 CC not bound as tightly by the reference protein. The non-antibody protein
 CC is useful as scaffolds for selecting or designing a protein framework
 CC with specific and favourable properties, e.g. for binding any antigen of
 CC interest, or for destroying or inactivating antibody molecules. The non-
 CC antibody protein is also useful in all areas where antibodies are used,
 CC e.g. research, therapeutic or diagnostic fields, and for screening novel
 CC binding proteins useful in the above-mentioned fields. The present
 CC proteins have thermodynamic properties superior to those of natural
 CC antibodies, and can be evolved rapidly in vitro. The present proteins or
 CC antibody mimics exhibit improved biophysical properties, such as
 CC stability under reducing conditions and solubility at high
 CC concentrations. In addition, these molecules are readily expressed and
 CC folded in prokaryotic systems (e.g. *Escherichia coli*), in eukaryotic
 CC systems (e.g. yeast), or in in vitro translation systems (e.g. rabbit
 CC reticulocyte lysate system). Furthermore, these proteins are extremely
 CC amenable to affinity maturation techniques involving multiple cycles of
 CC selection, e.g. in vitro selection using RNA-protein fusion technology,
 CC phage display or yeast display systems. The present sequence is used in
 CC the exemplification of the present invention

XX SQ Sequence 94 AA;

Query Match 99.0%; Score 489; DB 5; Length 94;
 Best Local Similarity 98.9%; Pred. No. 4.4e-49;
 Matches 93; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VSDVPRDLEVVAAATPTSRLLISWNRSGLQSRYYRITYTGTCGNSPVQEFVPPWASIAIS 60
 DB 1 VSDVPRDLEVVAAATPTSRLLISWNRSGLQSRYYRITYTGTCGNSPVQEFVPPWASIAIS 60

QY 61 GLKPGVDYITTVAVTDKSDTYKYDDPISINRYT 94

DB 61 GLKPGVDYITTVAVTDKSDTYKYDDPISINRYT 94

RESULT 5

ABB78920
 ID ABB78920 standard; peptide; 94 AA.

XX AC ABB78920;

DT 30-JUL-2002 (first entry)

XX Tumour necrosis factor-alpha binding amino acid sequence T14.23.

XX Protein scaffold; antibody; binding protein; immunoglobulin;
 KW tumour necrosis factor alpha; TNF-alpha; protein framework.

XX Homo sapiens.

OS Synthetic.

PN WO200232925-A2.

XX 25-APR-2002.

XX 16-OCT-2001; 2001WO-US032233.

XX 16-OCT-2000; 2000US-00688566.

XX (PHYL-) PHYLLOS INC.

XX Lipovsek D, Wagner RW, Kuimelis RG;

XX WPI; 2002-444238/47.

XX New non-antibody proteins having an immunoglobulin fold, useful in
 PT research, therapeutic or diagnostic fields, particularly as scaffolds for
 PT designing proteins with specific properties, e.g. for binding any antigen
 PT of interest.

XX New non-antibody proteins having an immunoglobulin fold, useful in
PT research, therapeutic or diagnostic fields, particularly as scaffolds for
PT designing proteins with specific properties, e.g. for binding any antigen
PT of interest.

XX Claim 47; Fig 25; 94pp; English.

XX The present invention describes a non-antibody protein, comprising a
CC domain having an immunoglobulin-like fold, derived from a reference
CC protein having a mutated amino acid sequence, where the non-antibody
CC protein binds with a Kd at least as tight as 10 nM to a compound that is
CC not bound as tightly by the reference protein. The non-antibody protein
CC is useful as scaffolds for selecting or designing a protein framework
CC with specific and favourable properties, e.g. for binding any antigen of
CC interest, or for destroying or inactivating antibody molecules. The non-
CC antibody protein is also useful in all areas where antibodies are used,
CC e.g. research, therapeutic or diagnostic fields, and for screening novel
CC binding proteins useful in the above-mentioned fields. The present
CC proteins have thermodynamic properties superior to those of natural
CC antibodies, and can be evolved rapidly in vitro. The present proteins or
CC antibody mimics exhibit improved biophysical properties, such as
CC stability under reducing conditions and solubility at high
CC concentrations. In addition, these molecules are readily expressed and
CC folded in prokaryotic systems (e.g. Escherichia coli), in eukaryotic
CC systems (e.g. yeast), or in in vitro translation systems (e.g. rabbit
CC reticulocyte lysate system). Furthermore, these proteins are extremely
CC amenable to affinity maturation techniques involving multiple cycles of
CC selection, e.g. in vitro selection using RNA-protein fusion technology,
CC phage display or yeast display systems. The present sequence is used in
CC the exemplification of the present invention

XX Sequence 94 AA;

Query Match 98.4%; Score 486; DB 5; Length 94;

Best Local Similarity 97.9%; Pred. No. 1e-48; Indels 0; Gaps 0;

Matches 92; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VSDVPRDLEVVAAATPTSLRLISWNRSLQSRYYRITYGTGNSPVQEFVPPWASIAIS 60

Db 1 LSDVPRDLEVVAAATPTSLRLISWNRSLQSRYYRITYGTGNSPVQEFVPPWASIAIS 60

Qy 61 GLKPGVDYTTITVAVTDKSDTYKYDDPISINYRT 94

Db 61 GLKPGVDYTTITVAVTDKSDTYKYDDPISINYRT 94

RESULT 8

ABB78940

ID ABB78940 standard; peptide; 94 AA.

XX AC ABB78940;

XX 30-JUL-2002 (first entry)

XX Tumour necrosis factor-alpha binding amino acid sequence M12.01.

XX Protein scaffold; antibody; binding protein; immunoglobulin;

KW tumour necrosis factor alpha; TNF-alpha; protein framework.

XX Homo sapiens.

OS Synthetic.

XX WO200232925-A2.

XX 25-APR-2002.

XX 16-OCT-2001; 2001WO-US032233.

XX 16-OCT-2000; 2000US-00688566.

XX (PHYL-) PHYLLOS INC.

PI Lipovsek D, Wagner RW, Kuimelis RG;

XX WPI; 2002-444238/47.

XX New non-antibody proteins having an immunoglobulin fold, useful in
PT research, therapeutic or diagnostic fields, particularly as scaffolds for
PT designing proteins with specific properties, e.g. for binding any antigen
PT of interest.

XX Claim 47; Fig 25; 94pp; English.

XX The present invention describes a non-antibody protein, comprising a
CC domain having an immunoglobulin-like fold, derived from a reference
CC protein having a mutated amino acid sequence, where the non-antibody
CC protein binds with a Kd at least as tight as 10 nM to a compound that is
CC not bound as tightly by the reference protein. The non-antibody protein
CC is useful as scaffolds for selecting or designing a protein framework
CC with specific and favourable properties, e.g. for binding any antigen of
CC interest, or for destroying or inactivating antibody molecules. The non-
CC antibody protein is also useful in all areas where antibodies are used,
CC e.g. research, therapeutic or diagnostic fields, and for screening novel
CC binding proteins useful in the above-mentioned fields. The present
CC proteins have thermodynamic properties superior to those of natural
CC antibodies, and can be evolved rapidly in vitro. The present proteins or
CC antibody mimics exhibit improved biophysical properties, such as
CC stability under reducing conditions and solubility at high
CC concentrations. In addition, these molecules are readily expressed and
CC folded in prokaryotic systems (e.g. Escherichia coli), in eukaryotic
CC systems (e.g. yeast), or in in vitro translation systems (e.g. rabbit
CC reticulocyte lysate system). Furthermore, these proteins are extremely
CC amenable to affinity maturation techniques involving multiple cycles of
CC selection, e.g. in vitro selection using RNA-protein fusion technology,
CC phage display or yeast display systems. The present sequence is used in
CC the exemplification of the present invention

XX Sequence 94 AA;

Query Match 98.0%; Score 484; DB 5; Length 94;

Best Local Similarity 96.8%; Pred. No. 1.7e-48; Indels 0; Gaps 0;

Matches 91; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VSDVPRDLEVVAAATPTSLRLISWNRSLQSRYYRITYGTGNSPVQEFVPPWASIAIS 60

Db 1 LSDVPRDLEVVAAATPTSLRLISWNRSLQSRYYRITYGTGNSPVQEFVPPWASIAIS 60

Qy 61 GLKPGVDYTTITVAVTDKSDTYKYDDPISINYRT 94

Db 61 GLKPGVDYTTITVAVTDKSDTYKYDDPISINYRT 94

RESULT 9

ABB78912

ID ABB78912 standard; peptide; 94 AA.

XX AC ABB78912;

XX 30-JUL-2002 (first entry)

XX Tumour necrosis factor-alpha binding amino acid sequence S08.03.

XX Protein scaffold; antibody; binding protein; immunoglobulin;

KW tumour necrosis factor alpha; TNF-alpha; protein framework.

XX Homo sapiens.

OS Synthetic.

XX WO200232925-A2.

XX 25-APR-2002.

XX 16-OCT-2001; 2001WO-US032233.

XX 16-OCT-2000; 2000US-00688566.

```
XX PA (PHYL-) PHYLOS INC.
XX PI Lipovsek D, Wagner RW, Kuimelis RG;
XX PI WPI; 2002-444238/47.
XX DR
XX PT New non-antibody proteins having an immunoglobulin fold, useful in
XX PT research, therapeutic or diagnostic fields, particularly as scaffolds for
XX PT designing proteins with specific properties, e.g. for binding any antigen
XX PT of interest.
XX PS Claim 47; Fig 25; 94pp; English.
XX CC The present invention describes a non-antibody protein, comprising a
XX CC domain having an immunoglobulin-like fold, derived from a reference
XX CC protein having a mutated amino acid sequence, where the non-antibody
XX CC protein binds with a Kd at least as tight as 10 nM to a compound that is
XX CC not bound as tightly by the reference protein. The non-antibody protein
XX CC is useful as scaffolds for selecting or designing a protein framework
XX CC with specific and favourable properties, e.g. for binding any antigen of
XX CC interest, or for destroying or inactivating antibody molecules. The non-
XX CC antibody protein is also useful in all areas where antibodies are used,
XX CC e.g. research, therapeutic or diagnostic fields, and for screening novel
XX CC binding proteins useful in the above-mentioned fields. The present
XX CC proteins have thermodynamic properties superior to those of natural
XX CC antibodies, and can be evolved rapidly in vitro. The present proteins or
XX CC antibody mimics exhibit improved biophysical properties, such as
XX CC stability under reducing conditions and solubility at high
XX CC concentrations. In addition, these molecules are readily expressed and
XX CC folded in prokaryotic systems (e.g. Escherichia coli), in eukaryotic
XX CC systems (e.g. yeast), or in in vitro translation systems (e.g. rabbit
XX CC reticulocyte lysate system). Furthermore, these proteins are extremely
XX CC amenable to affinity maturation techniques involving multiple cycles of
XX CC selection, e.g. in vitro selection using RNA-protein fusion technology,
XX CC phage display or yeast display systems. The present sequence is used in
XX CC the exemplification of the present invention
XX SQ Sequence 94 AA;
Query Match 98.0%; Score 484; DB 5; Length 94;
Best Local Similarity 97.9%; Pred. No. 1.7e-48;
Matches 92; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 VSDVPRDLEVVAATPTSLISNRSGLQSRYYRITYGETGNSPVQSEFTVPPWASTATIS 60
DB 1 VSDVPRDLEVVAATPTSLISNRSGLQSRYYRITYGETGNGPVGQSEFTVPPWASTATIS 60
QY 61 GLKPGVDYTIITVAVTDKSDTYKYDDPISINVRT 94
DB 61 GLKPGVDYTIITVAVTDMSDTYKYDDPISINVRT 94
RESULT 10
ABB78916
ID ABB78916 standard; peptide; 94 AA.
XX AC ABB78916;
XX DT 30-JUL-2002 (first entry)
XX DE Tumour necrosis factor-alpha binding amino acid sequence T14.13.
XX KW Protein scaffold; antibody; binding protein; immunoglobulin;
XX KW tumour necrosis factor alpha; TNF-alpha; protein framework.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO200232925-A2.
XX PD 25-APR-2002.
XX

PF 16-OCT-2001; 2001WO-US032233.
XX 16-OCT-2000; 2000US-00688566.
XX PA (PHYL-) PHYLOS INC.
XX PI Lipovsek D, Wagner RW, Kuimelis RG;
XX PI WPI; 2002-444238/47.
XX DR
XX PT New non-antibody proteins having an immunoglobulin fold, useful in
XX PT research, therapeutic or diagnostic fields, particularly as scaffolds for
XX PT designing proteins with specific properties, e.g. for binding any antigen
XX PT of interest.
XX PS Claim 47; Fig 25; 94pp; English.
XX CC The present invention describes a non-antibody protein, comprising a
XX CC domain having an immunoglobulin-like fold, derived from a reference
XX CC protein having a mutated amino acid sequence, where the non-antibody
XX CC protein binds with a Kd at least as tight as 10 nM to a compound that is
XX CC not bound as tightly by the reference protein. The non-antibody protein
XX CC is useful as scaffolds for selecting or designing a protein framework
XX CC with specific and favourable properties, e.g. for binding any antigen of
XX CC interest, or for destroying or inactivating antibody molecules. The non-
XX CC antibody protein is also useful in all areas where antibodies are used,
XX CC e.g. research, therapeutic or diagnostic fields, and for screening novel
XX CC binding proteins useful in the above-mentioned fields. The present
XX CC proteins have thermodynamic properties superior to those of natural
XX CC antibodies, and can be evolved rapidly in vitro. The present proteins or
XX CC antibody mimics exhibit improved biophysical properties, such as
XX CC stability under reducing conditions and solubility at high
XX CC concentrations. In addition, these molecules are readily expressed and
XX CC folded in prokaryotic systems (e.g. Escherichia coli), in eukaryotic
XX CC systems (e.g. yeast), or in in vitro translation systems (e.g. rabbit
XX CC reticulocyte lysate system). Furthermore, these proteins are extremely
XX CC amenable to affinity maturation techniques involving multiple cycles of
XX CC selection, e.g. in vitro selection using RNA-protein fusion technology,
XX CC phage display or yeast display systems. The present sequence is used in
XX CC the exemplification of the present invention
XX SQ Sequence 94 AA;
Query Match 97.8%; Score 483; DB 5; Length 94;
Best Local Similarity 97.9%; Pred. No. 2.2e-48;
Matches 92; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 VSDVPRDLEVVAATPTSLISNRSGLQSRYYRITYGETGNSPVQSEFTVPPWASTATIS 60
DB 1 VSDVPRDLEVVAATPTSLISNRSGLQSRYYRITYGETGNSPVQSEFTVPPWASTATIS 60
QY 61 GLKPGVDYTIITVAVTDKSDTYKYDDPISINVRT 94
DB 61 GLKPGVDYTIITVAVTDKSDTYKYDDPISINVRT 94
RESULT 11
ABB78918
ID ABB78918 standard; peptide; 94 AA.
XX AC ABB78918;
XX DT 30-JUL-2002 (first entry)
XX DE Tumour necrosis factor-alpha binding amino acid sequence T14.05.
XX KW Protein scaffold; antibody; binding protein; immunoglobulin;
XX KW tumour necrosis factor alpha; TNF-alpha; protein framework.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO200232925-A2.
XX PD 25-APR-2002.
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OM protein - protein search, using sw model

Run on: February 23, 2006, 07:47:49 ; Search time 47 Seconds
(without alignments)
165.351 Million cell updates/sec

Title: US-09-688-566-81

Perfect score: 494

Sequence: 1 VSDVPRDLEVAATPTSRLLI.....VTDKSDTYKYDDPISINVRT 94

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5 COMB.pap.*
- 2: /cgn2_6/ptodata/1/iaa/6 COMB.pap.*
- 3: /cgn2_6/ptodata/1/iaa/H COMB.pap.*
- 4: /cgn2_6/ptodata/1/iaa/PCITUS COMB.pap.*
- 5: /cgn2_6/ptodata/1/iaa/RE COMB.pap.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	361	73.1	94	1	US-08-717-169-8
2	361	73.1	94	2	US-09-638-202A-110
3	361	73.1	94	2	US-09-228-901A-8
4	361	73.1	94	2	US-09-096-749A-110
5	361	73.1	94	2	US-09-637-614-110
6	361	73.1	96	2	US-09-638-202A-112
7	361	73.1	96	2	US-09-096-749A-112
8	361	73.1	96	2	US-09-637-614-112
9	361	73.1	175	1	US-08-078-683A-34
10	361	73.1	175	2	US-08-471-970A-34
11	361	73.1	175	2	US-08-723-677B-34
12	361	73.1	256	1	US-07-959-369-1
13	361	73.1	258	1	US-07-959-369-10
14	361	73.1	274	1	US-07-959-369-12
15	361	73.1	274	1	US-08-836-854-3
16	361	73.1	274	2	US-09-366-009-25
17	361	73.1	274	2	US-08-809-156B-25
18	361	73.1	274	2	US-09-775-964-25
19	361	73.1	277	1	US-07-959-369-3
20	361	73.1	279	1	US-07-959-369-11
21	361	73.1	279	1	US-08-836-854-8
22	361	73.1	281	1	US-07-959-369-4
23	361	73.1	283	1	US-07-959-369-13
24	361	73.1	283	1	US-08-836-854-7
25	361	73.1	302	1	US-08-836-854-5
26	361	73.1	302	2	US-09-366-009-29
27	361	73.1	302	2	US-08-809-156B-29

28	361	73.1	302	2	US-09-775-964-29	Sequence 29, Appl
29	361	73.1	332	1	US-08-836-854-13	Sequence 13, Appl
30	361	73.1	341	1	US-08-836-854-14	Sequence 14, Appl
31	361	73.1	367	1	US-08-836-854-18	Sequence 18, Appl
32	361	73.1	368	1	US-08-836-854-17	Sequence 17, Appl
33	361	73.1	383	1	US-07-959-369-5	Sequence 5, Appl
34	361	73.1	385	1	US-07-959-369-14	Sequence 14, Appl
35	361	73.1	385	1	US-08-836-854-10	Sequence 10, Appl
36	361	73.1	422	1	US-08-836-854-12	Sequence 12, Appl
37	361	73.1	432	1	US-07-959-369-8	Sequence 8, Appl
38	361	73.1	432	1	US-07-959-369-9	Sequence 9, Appl
39	361	73.1	432	1	US-08-836-854-20	Sequence 20, Appl
40	361	73.1	432	2	US-09-366-009-4	Sequence 4, Appl
41	361	73.1	432	2	US-08-809-156B-4	Sequence 4, Appl
42	361	73.1	432	2	US-09-775-964-4	Sequence 4, Appl
43	361	73.1	446	1	US-08-836-854-15	Sequence 15, Appl
44	361	73.1	457	1	US-08-836-854-16	Sequence 16, Appl
45	361	73.1	457	2	US-09-366-009-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1

US-08-717-169-8

; Sequence 8, Application US/08717169

; Patent No. 5924676

; GENERAL INFORMATION:

; APPLICANT: Pasqualini, Renata

; APPLICANT: Ruoslahti, Erkki

; TITLE OF INVENTION: Methods of Inhibiting Angiogenesis and

; TITLE OF INVENTION: Ameliorating Cancer By Using Superfibronection

; NUMBER OF SEQUENCES: 18

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Campbell & Flores LLP

; STREET: 4370 La Jolla Village Drive, Suite 700

; CITY: San Diego

; STATE: California

; COUNTRY: USA

; ZIP: 92122

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/717,169

; FILING DATE: 20-SEP-1996

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: Campbell, Cathryn A.

; REGISTRATION NUMBER: 31,815

; REFERENCE/DOCKET NUMBER: P-LJ 2017

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (619) 535-9001

; TELEFAX: (619) 535-8949

; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 94 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; US-08-717-169-8

Query Match 73.1%; Score 361; DB 1; Length 94;

Best Local Similarity 77.7%; Pred. No. 1.8e-35;

Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

Qy 1 VSDVPRDLEVAATPTSRLLISWNRSGLSQSYRITYTGTSNPSVQETPPWASIAIIS 60

Db 1 VSDVPRDLEVAATPTSRLLISWNRSGLSQSYRITYTGTSNPSVQETPPWASIAIIS 60

QY 61 GLKPGVDYITTVYAVTDKSDTYKYDDPISINVRT 94
| | | | | | | | | | | | | | : | : | | | | |
Db 61 GLKPGVDYITTVYAVTGRGDPASSKRPISINVRT 94

RESULT 2

US-09-638-202A-110
; Sequence 110, Application US/09638202A
; Patent No. 6462189
; GENERAL INFORMATION:
; APPLICANT: Koieda, Shohei
; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
; NUMBER OF SEQUENCES: 118
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A.
; STREET: 121 South Eighth Street, Ste. 1600
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402

COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/638,202A
; FILING DATE: 11-Aug-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/096,749
; FILING DATE: <unknown>

ATTORNEY/AGENT INFORMATION:
; NAME: Ann S. Viksnins
; REGISTRATION NUMBER: 37,748
; REFERENCE/DOCKET NUMBER: 109.034US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (612) 373-6900
; TELEFAX: (612) 339-3061
; INFORMATION FOR SEQ ID NO: 110:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 94 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; SEQUENCE DESCRIPTION: SEQ ID NO: 110:

US-09-638-202A-110
Query Match 73.1%; Score 361; DB 2; Length 94;
Best Local Similarity 77.7%; Pred. No. 1.8e-35;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

QY 1 VSDVPRDLEVAATPTSLISWNRSLQSRYYRITYGETGNSPVQSFVTPPWASTATIS 60
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Db 1 VSDVPRDLEVAATPTSLISWNRSLQSRYYRITYGETGNSPVQSFVTPPWASTATIS 60

QY 61 GLKPGVDYITTVYAVTDKSDTYKYDDPISINVRT 94
| | | | | | | | | | | | | | : | : | | | | |
Db 61 GLKPGVDYITTVYAVTGRGDPASSKRPISINVRT 94

RESULT 3
US-09-228-901A-8
; Sequence 8, Application US/09228901A
; Patent No. 6475488
; GENERAL INFORMATION:
; APPLICANT: Pasqualini, Renata
; APPLICANT: Ruoslahti, Erkki I.
; TITLE OF INVENTION: Methods of Inhibiting Angiogenesis and

US-09-638-202A-110
Query Match 73.1%; Score 361; DB 2; Length 94;
Best Local Similarity 77.7%; Pred. No. 1.8e-35;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

QY 1 VSDVPRDLEVAATPTSLISWNRSLQSRYYRITYGETGNSPVQSFVTPPWASTATIS 60
| | | | | | | | | | | | | | : | : | | | | |
Db 1 VSDVPRDLEVAATPTSLISWNRSLQSRYYRITYGETGNSPVQSFVTPPWASTATIS 60

QY 61 GLKPGVDYITTVYAVTDKSDTYKYDDPISINVRT 94
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Db 61 GLKPGVDYITTVYAVTGRGDPASSKRPISINVRT 94

RESULT 4
US-09-096-749A-110
; Sequence 110, Application US/09096749A
; Patent No. 6673901
; GENERAL INFORMATION:
; APPLICANT: Koieda, Shohei
; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
; NUMBER OF SEQUENCES: 118
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A.
; STREET: 121 South Eighth Street, Ste. 1600
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402

COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/096,749A
; FILING DATE: June 12, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ann S. Viksnins
; REGISTRATION NUMBER: 37,748
; REFERENCE/DOCKET NUMBER: 109.034US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (612) 373-6900
; TELEFAX: (612) 339-3061
; INFORMATION FOR SEQ ID NO: 110:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 94 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORIGINAL SOURCE:
US-09-096-749A-110

; TITLE OF INVENTION: Ameliorating Cancer by Using Superfibronectin
; FILE REFERENCE: P-TX 3416
; CURRENT APPLICATION NUMBER: US/09/228,901A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 08/717,169
; PRIOR FILING DATE: 1996-09-20
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 94
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-228-901A-8

Query Match 73.1%; Score 361; DB 2; Length 94;
Best Local Similarity 77.7%; Pred. No. 1.8e-35;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

QY 1 VSDVPRDLEVAATPTSLISWNRSLQSRYYRITYGETGNSPVQSFVTPPWASTATIS 60
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Db 1 VSDVPRDLEVAATPTSLISWNRSLQSRYYRITYGETGNSPVQSFVTPPWASTATIS 60

QY 61 GLKPGVDYITTVYAVTDKSDTYKYDDPISINVRT 94
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Db 61 GLKPGVDYITTVYAVTGRGDPASSKRPISINVRT 94

RESULT 4
US-09-096-749A-110
; Sequence 110, Application US/09096749A
; Patent No. 6673901
; GENERAL INFORMATION:
; APPLICANT: Koieda, Shohei
; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
; NUMBER OF SEQUENCES: 118
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A.
; STREET: 121 South Eighth Street, Ste. 1600
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402

COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/096,749A
; FILING DATE: June 12, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ann S. Viksnins
; REGISTRATION NUMBER: 37,748
; REFERENCE/DOCKET NUMBER: 109.034US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (612) 373-6900
; TELEFAX: (612) 339-3061
; INFORMATION FOR SEQ ID NO: 110:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 94 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORIGINAL SOURCE:
US-09-096-749A-110


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; FRAGMENT TYPE: internal
US-08-078-683A-34

Query Match      73.1%; Score 361; DB 1; Length 175;
Best Local Similarity 77.7%; Pred. No. 4.2e-35;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

Qy 1 VSDVPRDLEVVAAFTPTSLRLISWNRSGLSQRYRITYTGETGNSPVQSFVPPWASIIATIS 60
Db 82 VSDVPRDLEVVAAFTPTSLRLISWNRSGLSQRYRITYTGETGNSPVQSFVPPWASIIATIS 141

Qy 61 GLKPGVDYTTITVAVTDKSDTYKYDDPISINRYT 94
Db 142 GLKPGVDYTTITVAVTGRGDSPASSKPIISINRYT 175

RESULT 10
US-08-471-970A-34
; Sequence 34, Application US/08471970A
; Patent No. 6531295
; GENERAL INFORMATION:
; APPLICANT: Saunders, Scott
; APPLICANT: Bernfield, Merton
; APPLICANT: Kato, Masato
; TITLE OF INVENTION: Construction and Use of Synthetic
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII (text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,970A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/078,683
; FILING DATE: 17-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kara, Catherine J.
; REGISTRATION NUMBER: P-41,106
; REFERENCE/DOCKET NUMBER: CME-062DV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-471-970A-34

Query Match      73.1%; Score 361; DB 2; Length 175;
Best Local Similarity 77.7%; Pred. No. 4.2e-35;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

Qy 1 VSDVPRDLEVVAAFTPTSLRLISWNRSGLSQRYRITYTGETGNSPVQSFVPPWASIIATIS 60
Db 82 VSDVPRDLEVVAAFTPTSLRLISWNRSGLSQRYRITYTGETGNSPVQSFVPPWASIIATIS 141

Qy 61 GLKPGVDYTTITVAVTDKSDTYKYDDPISINRYT 94
Db 142 GLKPGVDYTTITVAVTGRGDSPASSKPIISINRYT 175

; FRAGMENT TYPE: internal
US-09-723-677B-34
; Sequence 34, Application US/09723677B
; Patent No. 6699968
; GENERAL INFORMATION:
; APPLICANT: SAUNDERS, SCOTT
; APPLICANT: BERNFIELD, MERTON
; APPLICANT: KATO, MASATO
; TITLE OF INVENTION: CONSTRUCTION AND USE OF SYNTHETIC CONSTRUCTS ENCODING SYNDECAN
; FILE REFERENCE: 101353-151
; CURRENT APPLICATION NUMBER: US/09/723,677B
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 08/471,970
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: 08/078,683
; PRIOR FILING DATE: 1993-06-17
; PRIOR APPLICATION NUMBER: 07/856,869
; PRIOR FILING DATE: 1992-03-24
; PRIOR APPLICATION NUMBER: 07/757,654
; PRIOR FILING DATE: 1991-09-06
; PRIOR APPLICATION NUMBER: 07/746,797
; PRIOR FILING DATE: 1991-08-12
; PRIOR APPLICATION NUMBER: 07/331,585
; PRIOR FILING DATE: 1989-03-29
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 34
; LENGTH: 175
; TYPE: PRT
; ORGANISM: MUS SP;HOMO SAPIEN
US-09-723-677B-34

Query Match      73.1%; Score 361; DB 2; Length 175;
Best Local Similarity 77.7%; Pred. No. 4.2e-35;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

Qy 1 VSDVPRDLEVVAAFTPTSLRLISWNRSGLSQRYRITYTGETGNSPVQSFVPPWASIIATIS 60
Db 82 VSDVPRDLEVVAAFTPTSLRLISWNRSGLSQRYRITYTGETGNSPVQSFVPPWASIIATIS 141

Qy 61 GLKPGVDYTTITVAVTDKSDTYKYDDPISINRYT 94
Db 142 GLKPGVDYTTITVAVTGRGDSPASSKPIISINRYT 175

RESULT 12
US-07-959-369-1
; Sequence 1, Application US/07959369
; Patent No. 5302701
; GENERAL INFORMATION:
; APPLICANT: Hidetaka HASHI et al.
; TITLE OF INVENTION: No. 5302701el Functional Polypeptide
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/959,369
; FILING DATE: 19921013
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 274 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-836-854-3

Query Match 73.1%; Score 361; DB 1; Length 274;
Best Local Similarity 77.7%; Pred. No. 7.6e-35;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

QY 1 VSDVPRDLEVVAATPTSRLLISWNRSLQSRYYRITYTGETGNSPVQEFVPPWASITATIS 60
Db 178 VSDVPRDLEVVAATPTSRLLISWDAVTVVRYRITYTGETGNSPVQEFVPGSKSTATIS 237

QY 61 GLKPGVDYITITVAVTDKSDTYKYDDPISINYRT 94
Db 238 GLKPGVDYITITVAVTGRGDSPASSKPISINYRT 271

Search completed: February 23, 2006, 07:49:09
Job time : 47 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 23, 2006, 07:59:05 ; Search time 165 Seconds
(without alignments)
238.036 Million cell updates/sec

Title: US-09-688-566-81

Perfect score: 494

Sequence: 1 VSDVPRDLEVAATPTSRLLI.....VTDKSDTYKYDDPISINVRT 94

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Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA_Main:*

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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	361	73.1	94	3	US-09-096-749A-110
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4	361	73.1	94	4	US-10-165-155-110
5	361	73.1	94	4	US-10-190-162-110
6	361	73.1	94	5	US-10-509-055-3
7	361	73.1	96	3	US-09-096-749A-112
8	361	73.1	96	3	US-09-903-412-110
9	361	73.1	96	3	US-09-903-412-112
10	361	73.1	96	3	US-09-903-412-121
11	361	73.1	96	4	US-10-174-717A-112
12	361	73.1	96	4	US-10-165-155-112
13	361	73.1	96	4	US-10-190-162-112
14	361	73.1	96	4	US-10-006-760-2
15	361	73.1	175	5	US-10-776-989-34
16	361	73.1	184	5	US-10-895-590-2
17	361	73.1	184	5	US-10-895-590-4
18	361	73.1	184	5	US-10-895-590-6
19	361	73.1	274	3	US-09-775-964-25
20	361	73.1	274	5	US-10-486-512-1
21	361	73.1	274	5	US-10-509-055-8
22	361	73.1	302	3	US-09-775-964-29
23	361	73.1	302	5	US-10-486-512-7
24	361	73.1	302	5	US-10-509-055-13
25	361	73.1	330	4	US-10-279-733-10
26	361	73.1	367	5	US-10-486-512-8
27	361	73.1	367	5	US-10-509-055-14

28	361	73.1	368	5	US-10-486-512-9	Sequence 9, Appli
29	361	73.1	368	5	US-10-509-055-15	Sequence 15, Appl
30	361	73.1	370	5	US-10-486-512-10	Sequence 10, Appl
31	361	73.1	370	5	US-10-509-055-16	Sequence 16, Appl
32	361	73.1	432	3	US-09-775-964-4	Sequence 4, Appli
33	361	73.1	432	3	US-09-775-964-5	Sequence 5, Appli
34	361	73.1	457	3	US-09-775-964-22	Sequence 22, Appl
35	361	73.1	457	3	US-10-486-512-11	Sequence 11, Appl
36	361	73.1	457	5	US-10-509-055-17	Sequence 17, Appl
37	361	73.1	459	5	US-10-509-055-18	Sequence 18, Appl
38	361	73.1	464	3	US-09-775-964-7	Sequence 7, Appli
39	361	73.1	472	3	US-09-775-964-21	Sequence 21, Appl
40	361	73.1	472	5	US-10-486-512-12	Sequence 12, Appl
41	361	73.1	489	3	US-09-775-964-8	Sequence 8, Appli
42	361	73.1	489	3	US-09-775-964-23	Sequence 23, Appl
43	361	73.1	549	5	US-10-486-512-5	Sequence 5, Appli
44	361	73.1	549	5	US-10-509-055-11	Sequence 11, Appl
45	361	73.1	574	3	US-09-775-964-24	Sequence 24, Appl

ALIGNMENTS

RESULT 1
US-10-302-456-1
; Sequence 1, Application US/10302456
; Publication No. US20030100004A1
; GENERAL INFORMATION:
; APPLICANT: Kurz, Markus
; TITLE OF INVENTION: Solid Phase Immobilization of Proteins
; TITLE OF INVENTION: and Peptides
; FILE REFERENCE: 50036/051002
; CURRENT APPLICATION NUMBER: US/10/302,456
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/333,470
; PRIOR FILING DATE: 2001-11-27
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-302-456-1

Query Match 74.4%; Score 367.5; DB 4; Length 96;
Best Local Similarity 80.0%; Pred. No. 5.8e-34;
Matches 76; Conservative 3; Mismatches 15; Indels 1; Gaps 1;
Qy 1 VSDVPRDLEVAATPTSRLLISWNRSGLOSRYRITYTGCTGNSPVQSFVPPWASIATIS 60
Db 2 VSDVPRDLEVAATPTSRLLISWNRSGLOSRYRITYTGCTGNSPVQSFVPPWASIATIS 61
Qy 61 GLKPGVDYTTIVYAVTDKSDT-YKYDDPISINVRT 94
Db 62 GLKPGVDYTTIVYAVTPLRWTEAHPIPIINVRT 96

RESULT 2
US-09-096-749A-110
; Sequence 110, Application US/09096749A
; Patent No. US20020019517A1
; GENERAL INFORMATION:
; APPLICANT: Koleda, Shohel
; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
; NUMBER OF SEQUENCES: 118
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A.
; STREET: 121 South Eighth Street, Ste. 1600
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA

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;
;
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/096,749A
; FILING DATE: June 12, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ann S. Viksnins
; REGISTRATION NUMBER: 37,748
; REFERENCE/DOCKET NUMBER: 109.034US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (612) 373-6900
; TELEFAX: (612) 339-3061
; INFORMATION FOR SEQ ID NO: 110:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 94 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; SEQUENCE DESCRIPTION: SEQ ID NO: 110:
US-09-096-749A-110

Query Match 73.1%; Score 361; DB 3; Length 94;
Best Local Similarity 77.7%; Pred. No. 3.1e-33;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

QY 1 VSDVPRDLEVAATPTSLISWNRSGLOSYRYITYGETGNSPVQEFVTPPHASATIS 60
Db 1 VSDVPRDLEVAATPTSLISWNRSGLOSYRYITYGETGNSPVQEFVTPPHASATIS 60
QY 61 GLKPGVDYITTVYAVTDKSDTYKYDDPISINYRT 94
Db 61 GLKPGVDYITTVYAVTGRGDSPASSXPISINYRT 94

US-09-096-749A-110

Query Match 73.1%; Score 361; DB 3; Length 94;
Best Local Similarity 77.7%; Pred. No. 3.1e-33;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

QY 1 VSDVPRDLEVAATPTSLISWNRSGLOSYRYITYGETGNSPVQEFVTPPHASATIS 60
Db 1 VSDVPRDLEVAATPTSLISWNRSGLOSYRYITYGETGNSPVQEFVTPPHASATIS 60
QY 61 GLKPGVDYITTVYAVTDKSDTYKYDDPISINYRT 94
Db 61 GLKPGVDYITTVYAVTGRGDSPASSXPISINYRT 94

US-09-096-749A-110

RESULT 3
US-10-174-717A-110
; Sequence 110, Application US/10174717A
; Publication No. US20030108948A1
; APPLICANT: Koide, Shohei
; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
; NUMBER OF SEQUENCES: 118
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A.
; STREET: 121 South Eighth Street, St. 1600
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: WINDOWS
; SOFTWARE: FastSeq Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/174,717A
; FILING DATE: 18-Jun-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/096,749
; FILING DATE: June 12, 1998
; APPLICATION NUMBER: 60/049,410
; FILING DATE: June 12, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ann S. Viksnins
; REGISTRATION NUMBER: 37,748
; REFERENCE/DOCKET NUMBER: 109.034US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (612) 373-6900
; TELEFAX: (612) 339-3061
; INFORMATION FOR SEQ ID NO: 110:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 94 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
```

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;
;
; NAME: Ann S. Viksnins
; REGISTRATION NUMBER: 37,748
; REFERENCE/DOCKET NUMBER: 109.034US4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (612) 373-6900
; TELEFAX: (612) 339-3061
; INFORMATION FOR SEQ ID NO: 110:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 94 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; SEQUENCE DESCRIPTION: SEQ ID NO: 110:
US-10-174-717A-110

Query Match 73.1%; Score 361; DB 4; Length 94;
Best Local Similarity 77.7%; Pred. No. 3.1e-33;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

QY 1 VSDVPRDLEVAATPTSLISWNRSGLOSYRYITYGETGNSPVQEFVTPPHASATIS 60
Db 1 VSDVPRDLEVAATPTSLISWNRSGLOSYRYITYGETGNSPVQEFVTPPHASATIS 60
QY 61 GLKPGVDYITTVYAVTDKSDTYKYDDPISINYRT 94
Db 61 GLKPGVDYITTVYAVTGRGDSPASSXPISINYRT 94

US-10-165-155-110
RESULT 4
US-10-165-155-110
; Sequence 110, Application US/10165155
; Publication No. US20030134386A1
; GENERAL INFORMATION:
; APPLICANT: Koide, Shohei
; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
; NUMBER OF SEQUENCES: 118
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A.
; STREET: 121 South Eighth Street, Ste. 1600
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/165,155
; FILING DATE: 06-Jun-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/096,749
; FILING DATE: June 12, 1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Ann S. Viksnins
; REGISTRATION NUMBER: 37,748
; REFERENCE/DOCKET NUMBER: 109.034US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (612) 373-6900
; TELEFAX: (612) 339-3061
; INFORMATION FOR SEQ ID NO: 110:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 94 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
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;
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; SEQUENCE DESCRIPTION: SEQ ID NO: 110:
US-10-165-155-110

Query Match 73.1%; Score 361; DB 4; Length 94;
Best Local Similarity 77.7%; Pred. No. 3.le-33;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

QY 1 VSDPRDLEVVAATPTSRLLSNRSGLOSRYYRITYGETGNSPVQSFVPPWASIATIS 60
Db 1 VSDPRDLEVVAATPTSRLLSNRSGLOSRYYRITYGETGNSPVQSFVPPWASIATIS 60
QY 61 GLKPGVDYTTVYAVTDKSDTYKYDDPISINRYT 94
Db 61 GLKPGVDYTTVYAVTGRGDSPASSKFPISINRYT 94

RESULT 5
US-10-190-162-110
; Sequence 110, Application US/10190162
; Publication No. US2003017053A1
; GENERAL INFORMATION:
; APPLICANT: Koleda, Shohei
; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
; NUMBER OF SEQUENCES: 118
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A.
; STREET: 121 South Eighth Street, Ste. 1600
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/190,162
; FILING DATE: 03-Jul-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/096,749
; FILING DATE: June 12, 1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Ann S. Vikensins
; REGISTRATION NUMBER: 37,748
; REFERENCE/DOCKET NUMBER: 109.034US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (612) 373-6900
; TELEFAX: (612) 339-3061
; INFORMATION FOR SEQ ID NO: 110:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 94 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; SEQUENCE DESCRIPTION: SEQ ID NO: 110:
US-10-190-162-110

Query Match 73.1%; Score 361; DB 4; Length 94;
Best Local Similarity 77.7%; Pred. No. 3.le-33;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

QY 1 VSDPRDLEVVAATPTSRLLSNRSGLOSRYYRITYGETGNSPVQSFVPPWASIATIS 60

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Db      1  VSDVPRDLEVVAATPTSLISWDAPAVTVRYRITYTGETGCGNSPVQEFVTPGSKSTATIS 60
Qy      61  GLKPGVDYITITVYAVTDKSDTYKYDDPISINYRT 94
          ||||| : : |||||
Db      61  GLKPGVDYITITVYAVTGRGDSPASSKPI SINYRT 94
          ||||| : : |||||

RESULT 6
US-10-509-055-3
; Sequence 3, Application US/10509055
; Publication No. US20050227354A1
; GENERAL INFORMATION:
; APPLICANT: SAGAWA, Hiroaki et al.
; TITLE OF INVENTION: PROCESS FOR PRODUCING CYTOTOXIC LYMPHOCYTE
; FILE REFERENCE: 1422-0644PUS1
; CURRENT APPLICATION NUMBER: US/10/509,055
; CURRENT FILING DATE: 2004-09-24
; PRIOR APPLICATION NUMBER: PCT/JP03/03575
; PRIOR FILING DATE: 2003-03-25
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent-In 3.3
; SEQ ID NO 3
; LENGTH: 94
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: partial region of fibronectin named III-10
US-10-509-055-3

Query Match 73.1%; Score 361, DB 5, Length 94;
Best Local Similarity 77.7%; Pred. No. 3.le-33;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

Qy      1  VSDVPRDLEVVAATPTSLISWNRSGLQSRYYRITYTGETGCGNSPVQEFVTPPWASITATIS 60
Db      1  VSDVPRDLEVVAATPTSLISWDAPAVTVRYRITYTGETGCGNSPVQEFVTPGSKSTATIS 60
          ||||| : : |||||
Qy      61  GLKPGVDYITITVYAVTDKSDTYKYDDPISINYRT 94
          ||||| : : |||||
Db      61  GLKPGVDYITITVYAVTGRGDSPASSKPI SINYRT 94
          ||||| : : |||||

RESULT 7
US-09-096-749A-112
; Sequence 112, Application US/09096749A
; Patent No. US20020019517A1
; GENERAL INFORMATION:
; APPLICANT: Koleda, Shohei
; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
; NUMBER OF SEQUENCES: 118
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A.
; STREET: 121 South Eighth Street, Ste. 1600
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/096,749A
; FILING DATE: June 12, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ann S. Viksnins
; REGISTRATION NUMBER: 37,748
; REFERENCE/DOCKET NUMBER: 109.034US1
; TELECOMMUNICATION INFORMATION:

```

```
; TELEPHONE: (612) 373-6900
; TELEFAX: (612) 339-3061
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 96 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; US-09-096-749A-112

Query Match 73.1%; Score 361; DB 3; Length 96;
Best Local Similarity 77.7%; Pred. No. 3.2e-33;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

QY 1 VSDVPRDLEVAATPTSLISWNRSGLSQRYRYRITYGETGNSPVQEFVPPWASITATIS 60
Db 3 VSDVPRDLEVAATPTSLISWNRSGLSQRYRYRITYGETGNSPVQEFVPPWASITATIS 62

QY 61 GLKPGVDYITTVAVTDKSDTYKYDDPISINYRT 94
Db 63 GLKPGVDYITTVAVTGRGDSPASSKPISINYRT 96

RESULT 8
US-09-903-412-110
; Sequence 110, Application US/09903412
; Publication No. US20030027319A1
; GENERAL INFORMATION:
; APPLICANT: Koide, Shohei
; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
; FILE REFERENCE: 109.050US1
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US/09/903,412
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US 60/217,474
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 110
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The synthetic Fn3 gene.
US-09-903-412-110

Query Match 73.1%; Score 361; DB 3; Length 96;
Best Local Similarity 77.7%; Pred. No. 3.2e-33;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

QY 1 VSDVPRDLEVAATPTSLISWNRSGLSQRYRYRITYGETGNSPVQEFVPPWASITATIS 60
Db 3 VSDVPRDLEVAATPTSLISWNRSGLSQRYRYRITYGETGNSPVQEFVPPWASITATIS 62

QY 61 GLKPGVDYITTVAVTDKSDTYKYDDPISINYRT 94
Db 63 GLKPGVDYITTVAVTGRGDSPASSKPISINYRT 96

RESULT 9
US-09-903-412-112
; Sequence 112, Application US/09903412
; Publication No. US20030027319A1
; GENERAL INFORMATION:
; APPLICANT: Koide, Shohei
; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
; FILE REFERENCE: 109.050US1
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US/09/903,412
; OTHER INFORMATION: The designed Fn3 gene.
US-09-903-412-112

Query Match 73.1%; Score 361; DB 3; Length 96;
Best Local Similarity 77.7%; Pred. No. 3.2e-33;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

QY 1 VSDVPRDLEVAATPTSLISWNRSGLSQRYRYRITYGETGNSPVQEFVPPWASITATIS 60
Db 3 VSDVPRDLEVAATPTSLISWNRSGLSQRYRYRITYGETGNSPVQEFVPPWASITATIS 62

QY 61 GLKPGVDYITTVAVTDKSDTYKYDDPISINYRT 94
Db 63 GLKPGVDYITTVAVTGRGDSPASSKPISINYRT 96

RESULT 10
US-09-903-412-121
; Sequence 121, Application US/09903412
; Publication No. US20030027319A1
; GENERAL INFORMATION:
; APPLICANT: Koide, Shohei
; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
; FILE REFERENCE: 109.050US1
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US/09/903,412
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US 60/217,474
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 121
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: The designed Fn3 gene.
US-09-903-412-121

Query Match 73.1%; Score 361; DB 3; Length 96;
Best Local Similarity 77.7%; Pred. No. 3.2e-33;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

QY 1 VSDVPRDLEVAATPTSLISWNRSGLSQRYRYRITYGETGNSPVQEFVPPWASITATIS 60
Db 3 VSDVPRDLEVAATPTSLISWNRSGLSQRYRYRITYGETGNSPVQEFVPPWASITATIS 62

QY 61 GLKPGVDYITTVAVTDKSDTYKYDDPISINYRT 94
Db 63 GLKPGVDYITTVAVTGRGDSPASSKPISINYRT 96

RESULT 11
US-10-174-717A-112
; Sequence 112, Application US/10174717A
; Publication No. US20030108948A1
; APPLICANT: Koide, Shohei
; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
; NUMBER OF SEQUENCES: 118
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A.
; STREET: 121 South Eighth Street, St. 1600
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
```



```

; NAME: Ann S. Vikensins
; REGISTRATION NUMBER: 37,748
; REFERENCE/DOCKET NUMBER: 109.034US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (612) 373-6900
; TELEFAX: (612) 339-3061
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 96 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; SEQUENCE DESCRIPTION: SEQ ID NO: 112:
US-10-165-153-112

Query Match 73.1%; Score 361; DB 4; Length 96;
Best Local Similarity 77.7%; Pred.No.3.2e-33;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

QY 1 VSDPRDLVVAATPSRLISWNRSGLQGRYYRITYTGETCGNSFVQBFTVPPWASIATIS 60
Db 3 VSDPRDLVVAATPSRLISWNRSGLQGRYYRITYTGETCGNSFVQBFTVPPWASIATIS 62
QY 61 GLKPGVDYITVYAVTKDSQTYKYDDPISINYET 94
Db 63 GLKPGVDYITVYAVTGRGDSPASSKRPISINYET 96

RESULT 13
US-10-190-162-112
; Sequence 112, Application US/10190162
; Publication No. US20030170753A1
; GENERAL INFORMATION:
; APPLICANT: Koieda, Shohei
; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
; NUMBER OF SEQUENCES: 118
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A.
; STREET: 121 South Eighth Street, Ste. 1600
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/190,162
; FILING DATE: 03-Jul-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/096,749
; FILING DATE: June 12, 1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Ann S. Vikensins
; REGISTRATION NUMBER: 37,748
; REFERENCE/DOCKET NUMBER: 109.034US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (612) 373-6900
; TELEFAX: (612) 339-3061
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 96 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

```

```
;
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; SEQUENCE DESCRIPTION: SEQ ID NO: 112:
US-10-190-162-112

Query Match          73.1%; Score 361; DB 4; Length 96;
Best Local Similarity 77.7%; Pred. No. 3.2e-33;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

QY 1 VSDVPRDLEVVAAATPTSLRLISWNRSGLQSRYYRITYTGETGNSPVQEFVPPWASITATIS 60
   ||||| ||||| ||||| ||||| : ||||| ||||| ||||| ||||| |||||
Db 3 VSDVPRDLEVVAAATPTSLRLISWDAPAVTVRYRITYTGETGNSPVQEFVPGSKSTATIS 62

QY 61 GLKPGVDYTIITVYAVTDKSDTYKYDDPISINYRT 94
   ||||| ||||| ||||| ||||| : ||||| ||||| ||||| |||||
Db 63 GLKPGVDYTIITVYAVTGRGDSPASSKPISINYRT 96

RESULT 14
US-10-006-760-2
; Sequence 2, Application US/10006760
; Publication No. US20030186385A1
; GENERAL INFORMATION:
; APPLICANT: Koide, Shohel
; TITLE OF INVENTION: METHOD OF IDENTIFYING POLYPEPTIDE MONOBODIES WHICH BIND
; FILE REFERENCE: 176/60901
; CURRENT APPLICATION NUMBER: US/10/006,760
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/249,756
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-006-760-2

Query Match          73.1%; Score 361; DB 4; Length 96;
Best Local Similarity 77.7%; Pred. No. 3.2e-33;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

QY 1 VSDVPRDLEVVAAATPTSLRLISWNRSGLQSRYYRITYTGETGNSPVQEFVPPWASITATIS 60
   ||||| ||||| ||||| ||||| : ||||| ||||| ||||| |||||
Db 3 VSDVPRDLEVVAAATPTSLRLISWDAPAVTVRYRITYTGETGNSPVQEFVPGSKSTATIS 62

QY 61 GLKPGVDYTIITVYAVTDKSDTYKYDDPISINYRT 94
   ||||| ||||| ||||| ||||| : ||||| ||||| ||||| |||||
Db 63 GLKPGVDYTIITVYAVTGRGDSPASSKPISINYRT 96

RESULT 15
US-10-776-989-34
; Sequence 34, Application US/10776989
; Publication No. US20050075484A1
; GENERAL INFORMATION:
; APPLICANT: SAUNDERS, SCOTT
; APPLICANT: BERNFIELD, NERTON
; APPLICANT: KATO, MASATO
; TITLE OF INVENTION: CONSTRUCTION AND USE OF SYNTHETIC CONSTRUCTS ENCODING SYNDECAN
; FILE REFERENCE: 101353-232
; CURRENT APPLICATION NUMBER: US/10/776,989
; CURRENT FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 09/723,677
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 08/471,970
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: 08/078,683
; PRIOR FILING DATE: 1993-06-17
; PRIOR APPLICATION NUMBER: 07/856,869
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; PRIOR FILING DATE: 1992-03-24
; PRIOR APPLICATION NUMBER: 07/757,654
; PRIOR FILING DATE: 1991-09-06
; PRIOR APPLICATION NUMBER: 07/746,797
; PRIOR FILING DATE: 1991-08-12
; PRIOR APPLICATION NUMBER: 07/331,585
; PRIOR FILING DATE: 1989-03-29
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 34
; LENGTH: 175
; TYPE: PRT
; ORGANISM: MUS SP;HOMO SAPIEN
US-10-776-989-34

Query Match          73.1%; Score 361; DB 5; Length 175;
Best Local Similarity 77.7%; Pred. No. 6.7e-33;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

QY 1 VSDVPRDLEVVAAATPTSLRLISWNRSGLQSRYYRITYTGETGNSPVQEFVPPWASITATIS 60
   ||||| ||||| ||||| ||||| : ||||| ||||| ||||| |||||
Db 82 VSDVPRDLEVVAAATPTSLRLISWDAPAVTVRYRITYTGETGNSPVQEFVPGSKSTATIS 141

QY 61 GLKPGVDYTIITVYAVTDKSDTYKYDDPISINYRT 94
   ||||| ||||| ||||| ||||| : ||||| ||||| ||||| |||||
Db 142 GLKPGVDYTIITVYAVTGRGDSPASSKPISINYRT 175

Search completed: February 23, 2006, 08:04:06
Job time : 166 secs
```



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; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 274 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: <Unknown>
;   TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-11-181-091-25

Query Match      73.1%; Score 361; DB 7; Length 274;
Best Local Similarity 77.7%; Pred. No. 4.4e-32;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

QY 1 VSDVPRDLEVAATPTSLRISNRSGLSQRYRYITYGETGCGNSPVQEFVTPPWASITATIS 60
Db 178 VSDVPRDLEVAATPTSLRISNDAPAVTVRYRYITYGETGCGNSPVQEFVTPGSKSTATIS 237
QY 61 GLKPGVDYITTVYAVTDKSDTYKYDDPISINYRT 94
Db 238 GLKPGVDYITTVYAVTGRGDSPASSKPIISINYRT 271

RESULT 2
US-11-181-091-29
; Sequence 29, Application US/11181091
; Publication No. US20060030046A1
; GENERAL INFORMATION:
; APPLICANT: Asada, Kiyozo
; Uemori, Takashi
; Koyama, Nobuto
; Hashino, Kimikazu
; Kato, Ikunoshin
; TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
; CELLS WITH RETROVIRUS
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WEISER & ASSOCIATES
; STREET: 230 South Fifteenth Street, Suite 500
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/181,091
; FILING DATE: 14-Jul-2005
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/775,964
; FILING DATE: 20-Feb-2001
; APPLICATION NUMBER: US/09/366,009
; FILING DATE: 02-Aug-1999
; APPLICATION NUMBER: 08/809,156
; FILING DATE: <Unknown>
; APPLICATION NUMBER: JP 294382/1995
; FILING DATE: 13-NOV-1995
; APPLICATION NUMBER: JP 051847/1996
; FILING DATE: 08-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Weiser, Gerard J.
; REGISTRATION NUMBER: 19,763
; REFERENCE/DOCKET NUMBER: 977.6507P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-875-8393
; TELEFAX: 215-875-8394
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 432 amino acids
;   TYPE: amino acid
```

```
; LENGTH: 302 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-11-181-091-29

Query Match      73.1%; Score 361; DB 7; Length 302;
Best Local Similarity 77.7%; Pred. No. 4.9e-32;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

QY 1 VSDVPRDLEVAATPTSLRISNRSGLSQRYRYITYGETGCGNSPVQEFVTPPWASITATIS 60
Db 178 VSDVPRDLEVAATPTSLRISNDAPAVTVRYRYITYGETGCGNSPVQEFVTPGSKSTATIS 237
QY 61 GLKPGVDYITTVYAVTDKSDTYKYDDPISINYRT 94
Db 238 GLKPGVDYITTVYAVTGRGDSPASSKPIISINYRT 271

RESULT 3
US-11-181-091-4
; Sequence 4, Application US/11181091
; Publication No. US20060030046A1
; GENERAL INFORMATION:
; APPLICANT: Asada, Kiyozo
; Uemori, Takashi
; Koyama, Nobuto
; Hashino, Kimikazu
; Kato, Ikunoshin
; TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
; CELLS WITH RETROVIRUS
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WEISER & ASSOCIATES
; STREET: 230 South Fifteenth Street, Suite 500
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/181,091
; FILING DATE: 14-Jul-2005
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/775,964
; FILING DATE: 20-Feb-2001
; APPLICATION NUMBER: US/09/366,009
; FILING DATE: 02-Aug-1999
; APPLICATION NUMBER: 08/809,156
; FILING DATE: <Unknown>
; APPLICATION NUMBER: JP 294382/1995
; FILING DATE: 13-NOV-1995
; APPLICATION NUMBER: JP 051847/1996
; FILING DATE: 08-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Weiser, Gerard J.
; REGISTRATION NUMBER: 19,763
; REFERENCE/DOCKET NUMBER: 977.6507P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-875-8393
; TELEFAX: 215-875-8394
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 432 amino acids
;   TYPE: amino acid
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```
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-11-181-091-4

Query Match      73.1%; Score 361; DB 7; Length 432;
Best Local Similarity 77.7%; Pred. No. 7.5e-32;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

Qy 1 VSDVPRDLEVVAAATPTSLISWNRSGLOSRYYRITYGETGNSPVQSFVPPWASIASIS 60
Db 178 VSDVPRDLEVVAAATPTSLISWDAVAVTVYRITYGETGNSPVQSFVPGSKSTATIS 237
Qy 61 GLKPGVDYTTIVYAVTDKSDTYKYDDPISINYRT 94
Db 238 GLKPGVDYTTIVYAVTGRGDSPASSKPFISINYRT 271

RESULT 4
US-11-181-091-5
; Sequence 5, Application US/11181091
; Publication No. US20060030046A1
; GENERAL INFORMATION:
; APPLICANT: Asada, Kiyozo
; Uemori, Takashi
; Ueno, Takashi
; Koyama, Nobuto
; Hashino, Kimikazu
; Kato, Ikunoshin
; TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
; CELLS WITH RETROVIRUS
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WEISER & ASSOCIATES
; STREET: 230 South Fifteenth Street, Suite 500
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/181,091
; FILING DATE: 14-Jul-2005
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/775,964
; FILING DATE: 20-Feb-2001
; APPLICATION NUMBER: US/09/366,009
; FILING DATE: 02-Aug-1999
; APPLICATION NUMBER: 08/809,156
; FILING DATE: <Unknown>
; APPLICATION NUMBER: JP 294382/1995
; FILING DATE: 13-NOV-1995
; APPLICATION NUMBER: JP 051847/1996
; FILING DATE: 08-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Weiser, Gerard J.
; REGISTRATION NUMBER: 19,763
; REFERENCE/DOCKET NUMBER: 977.6507P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-875-8383
; TELEFAX: 215-875-8394
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 457 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 22:

; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-11-181-091-5

Query Match      73.1%; Score 361; DB 7; Length 457;
Best Local Similarity 77.7%; Pred. No. 8e-32;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

Qy 1 VSDVPRDLEVVAAATPTSLISWNRSGLOSRYYRITYGETGNSPVQSFVPPWASIASIS 60
Db 178 VSDVPRDLEVVAAATPTSLISWDAVAVTVYRITYGETGNSPVQSFVPGSKSTATIS 237
Qy 61 GLKPGVDYTTIVYAVTDKSDTYKYDDPISINYRT 94
Db 238 GLKPGVDYTTIVYAVTGRGDSPASSKPFISINYRT 271

RESULT 5
US-11-181-091-22
; Sequence 22, Application US/11181091
; Publication No. US20060030046A1
; GENERAL INFORMATION:
; APPLICANT: Asada, Kiyozo
; Uemori, Takashi
; Ueno, Takashi
; Koyama, Nobuto
; Hashino, Kimikazu
; Kato, Ikunoshin
; TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
; CELLS WITH RETROVIRUS
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WEISER & ASSOCIATES
; STREET: 230 South Fifteenth Street, Suite 500
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/181,091
; FILING DATE: 14-Jul-2005
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/775,964
; FILING DATE: 20-Feb-2001
; APPLICATION NUMBER: US/09/366,009
; FILING DATE: 02-Aug-1999
; APPLICATION NUMBER: 08/809,156
; FILING DATE: <Unknown>
; APPLICATION NUMBER: JP 294382/1995
; FILING DATE: 13-NOV-1995
; APPLICATION NUMBER: JP 051847/1996
; FILING DATE: 08-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Weiser, Gerard J.
; REGISTRATION NUMBER: 19,763
; REFERENCE/DOCKET NUMBER: 977.6507P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-875-8383
; TELEFAX: 215-875-8394
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 457 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 22:
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US-11-181-091-22

Query Match 73.1%; Score 361; DB 7; Length 457;
Best Local Similarity 77.7%; Pred. No. 8e-32;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

QY 1 VSDVPRDLVVAATPTSLISWNRSGLQSYRYRITYGETGNSPVQEFVPPWASITATIS 60
DB 178 VSDVPRDLVVAATPTSLISWDAPAVTVRYRITYGETGNSPVQEFVPGSKSTATIS 237
QY 61 GLKPGVDYTTTVAVTGRGSDPASSKPIISINYRT 94
DB 238 GLKPGVDYTTTVAVTGRGSDPASSKPIISINYRT 271

RESULT 6

US-11-181-091-7
; Sequence 7, Application US/11181091
; Publication No. US20060030046A1

GENERAL INFORMATION:
APPLICANT: Asada, Kiyozo
Uemori, Takashi
Ueno, Takashi
Koyama, Nobuto
Hashino, Kimikazu
Kato, Ikunoshin

TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
CELLS WITH RETROVIRUS

NUMBER OF SEQUENCES: 39

CORRESPONDENCE ADDRESS:

ADDRESSEE: WEISER & ASSOCIATES
STREET: 230 South Fifteenth Street, Suite 500
CITY: Philadelphia
STATE: PA

COUNTRY: USA

ZIP: 19102

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/181,091
FILING DATE: 14-Jul-2005

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/775,964
FILING DATE: 20-Feb-2001
APPLICATION NUMBER: US/09/366,009
FILING DATE: 02-Aug-1999
APPLICATION NUMBER: 08/809,156
FILING DATE: <Unknown>
APPLICATION NUMBER: JP 294382/1995
FILING DATE: 13-NOV-1995
APPLICATION NUMBER: JP 051847/1996
FILING DATE: 08-MAR-1996

ATTORNEY/AGENT INFORMATION:

NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 977.6507P
TELEPHONE: 215-875-8383
TELEFAX: 215-875-8394

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:
LENGTH: 464 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 7:

US-11-181-091-7

Query Match 73.1%; Score 361; DB 7; Length 464;

Best Local Similarity 77.7%; Pred. No. 8.1e-32;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

QY 1 VSDVPRDLVVAATPTSLISWNRSGLQSYRYRITYGETGNSPVQEFVPPWASITATIS 60
DB 178 VSDVPRDLVVAATPTSLISWDAPAVTVRYRITYGETGNSPVQEFVPGSKSTATIS 237
QY 61 GLKPGVDYTTTVAVTGRGSDPYKYDDPISINYRT 94
DB 238 GLKPGVDYTTTVAVTGRGSDPASSKPIISINYRT 271

RESULT 7

US-11-181-091-21
; Sequence 21, Application US/11181091
; Publication No. US20060030046A1

GENERAL INFORMATION:

APPLICANT: Asada, Kiyozo
Uemori, Takashi
Ueno, Takashi
Koyama, Nobuto
Hashino, Kimikazu
Kato, Ikunoshin

TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
CELLS WITH RETROVIRUS

NUMBER OF SEQUENCES: 39

CORRESPONDENCE ADDRESS:

ADDRESSEE: WEISER & ASSOCIATES
STREET: 230 South Fifteenth Street, Suite 500
CITY: Philadelphia
STATE: PA

COUNTRY: USA

ZIP: 19102

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/181,091
FILING DATE: 14-Jul-2005

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/775,964
FILING DATE: 20-Feb-2001
APPLICATION NUMBER: US/09/366,009
FILING DATE: 02-Aug-1999
APPLICATION NUMBER: 08/809,156
FILING DATE: <Unknown>
APPLICATION NUMBER: JP 294382/1995
FILING DATE: 13-NOV-1995
APPLICATION NUMBER: JP 051847/1996
FILING DATE: 08-MAR-1996

ATTORNEY/AGENT INFORMATION:

NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 977.6507P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
TELEFAX: 215-875-8394

INFORMATION FOR SEQ ID NO: 21:

SEQUENCE CHARACTERISTICS:
LENGTH: 472 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 21:

US-11-181-091-21

Query Match 73.1%; Score 361; DB 7; Length 472;

Best Local Similarity 77.7%; Pred. No. 8.3e-32;

Db 178 VSDVPRDLEVAATPTSLISWDAPAVTVRYRITYTGETCGNSPVQEFVTPGSKSTATIS 237

Qy 61 GLKPGVDYTTIVYAVTDKSDTYKYDDPISINVRT 94
| | | | | : | : | | | | |
Db 238 GLKPGVDYTTIVYAVTGRGDSPASSKFPISINVRT 271

RESULT 10

US-11-181-091-24
; Sequence 24, Application US/11181091
; Publication No. US20060030046A1
; GENERAL INFORMATION:
; APPLICANT: Asada, Kiyozo
; Uemori, Takashi
; Koyama, Nobuto
; Hashino, Kimikazu
; Kato, Ikunoshin
; TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
; CELLS WITH RETROVIRUS
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WEISER & ASSOCIATES
; STREET: 230 South Fifteenth Street, Suite 500
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/181,091
; FILING DATE: 14-Jul-2005
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/775,964
; FILING DATE: 20-Feb-2001
; APPLICATION NUMBER: US/09/366,009
; FILING DATE: 02-Aug-1999
; APPLICATION NUMBER: 08/809,156
; FILING DATE: <Unknown>
; APPLICATION NUMBER: JP 294382/1995
; FILING DATE: 13-NOV-1995
; APPLICATION NUMBER: JP 051847/1996
; FILING DATE: 08-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Weiser, Gerard J.
; REGISTRATION NUMBER: 19,763
; REFERENCE/DOCKET NUMBER: 977.6507P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-875-8383
; TELEFAX: 215-875-8394
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 574 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-11-181-091-24

Query Match 73.1%; Score 361; DB 7; Length 574;
Best Local Similarity 77.7%; Pred. No. 1e-31;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

Qy 1 VSDVPRDLEVAATPTSLISWDAPAVTVRYRITYTGETCGNSPVQEFVTPPWSATIS 60
| | | | | : | : | | | | |
Db 178 VSDVPRDLEVAATPTSLISWDAPAVTVRYRITYTGETCGNSPVQEFVTPGSKSTATIS 237

Qy 61 GLKPGVDYTTIVYAVTDKSDTYKYDDPISINVRT 94
| | | | | : | : | | | | |
Db 238 GLKPGVDYTTIVYAVTGRGDSPASSKFPISINVRT 271

RESULT 11

US-11-181-091-14
; Sequence 14, Application US/11181091
; Publication No. US20060030046A1
; GENERAL INFORMATION:
; APPLICANT: Asada, Kiyozo
; Uemori, Takashi
; Koyama, Nobuto
; Hashino, Kimikazu
; Kato, Ikunoshin
; TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
; CELLS WITH RETROVIRUS
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WEISER & ASSOCIATES
; STREET: 230 South Fifteenth Street, Suite 500
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/181,091
; FILING DATE: 14-Jul-2005
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/775,964
; FILING DATE: 20-Feb-2001
; APPLICATION NUMBER: US/09/366,009
; FILING DATE: 02-Aug-1999
; APPLICATION NUMBER: 08/809,156
; FILING DATE: <Unknown>
; APPLICATION NUMBER: JP 294382/1995
; FILING DATE: 13-NOV-1995
; APPLICATION NUMBER: JP 051847/1996
; FILING DATE: 08-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Weiser, Gerard J.
; REGISTRATION NUMBER: 19,763
; REFERENCE/DOCKET NUMBER: 977.6507P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-875-8383
; TELEFAX: 215-875-8394
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 826 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-11-181-091-14

Query Match 73.1%; Score 361; DB 7; Length 826;
Best Local Similarity 77.7%; Pred. No. 1.6e-31;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

Qy 1 VSDVPRDLEVAATPTSLISWDAPAVTVRYRITYTGETCGNSPVQEFVTPPWSATIS 60
| | | | | : | : | | | | |
Db 181 VSDVPRDLEVAATPTSLISWDAPAVTVRYRITYTGETCGNSPVQEFVTPGSKSTATIS 240

Qy 61 GLKPGVDYTTIVYAVTDKSDTYKYDDPISINVRT 94
| | | | | : | : | | | | |

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